OM protein - protein search, using sw model

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GenCore version 5.1.7

Run on: March 21, 2006, 18:07:45 ; Search time 14.883 Seconds
(without alignments)
261.554 Million cell updates/sec

Title: US-10-768-193-7
Perfect score: 737
Sequence: 1 MGHWIFLFLLSGTAGVHSE...........RGANWVFDYWGQGTTLTVSS 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptcodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptcodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptcodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptcodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptcodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptcodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptcodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptcodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	571	77.5	115	7	US-11-165-023-16	Sequence 16, Appl
2	569.5	77.3	137	7	US-11-074-373-39	Sequence 39, Appl
3	558	75.3	115	7	US-11-165-023-31	Sequence 31, Appl
4	555	75.3	115	7	US-11-165-023-32	Sequence 32, Appl
5	541.5	73.5	592	6	US-10-016-686-4	Sequence 4, Appli
6	541	73.4	138	6	US-10-125-837-22	Sequence 22, Appl
7	539.5	73.2	139	6	US-10-504-389A-28	Sequence 28, Appl
8	526	71.4	140	7	US-11-193-512-27	Sequence 27, Appl
9	502	68.1	140	7	US-11-193-512-63	Sequence 63, Appl
10	501	68.0	153	7	US-11-250-411-88	Sequence 88, Appl
11	499.5	67.8	143	7	US-11-126-799-4	Sequence 4, Appli
12	498.5	67.8	293	6	US-10-932-334-52	Sequence 52, Appl
13	498.5	67.6	412	7	US-11-116-939-10	Sequence 10, Appl
14	498.5	67.6	824	7	US-11-116-939-12	Sequence 12, Appl
15	498.5	67.6		7	US-11-116-939-11	Sequence 11, Appl
16	494	67.0	142	7	US-11-170-453-7	Sequence 7, Appl
17	491	66.6	130	7	US-11-188-187A-3	Sequence 3, Appl
18	490	66.6	140	7	US-11-193-512-74	Sequence 74, Appl
19	490	66.3	488	6	US-10-016-686-3	Sequence 3, Appl
20	488.5	66.3	488	6	US-10-016-686-6	Sequence 6, Appl
21	488	66.1	462	7	US-11-177-644-9	Sequence 9, Appl
22	485	65.9	138	7	US-11-089-872-3	Sequence 3, Appl
23	485	65.8	140	7	US-11-183-205-62	Sequence 62, Appl
24	483.5	65.6	243	6	US-10-016-686-1	Sequence 1, Appl
25	482	65.6	136	7	US-11-250-411-91	Sequence 91, Appl
25	480.5	65.2	114	7	US-11-102-743-7	Sequence 7, Appl
26	480	65.1	119	7	US-11-097-812-71	Sequence 71, Appl
27	480	65.1	119	7	US-11-097-812-72	Sequence 72, Appl
28	480	65.1	119	7	US-11-097-812-73	Sequence 73, Appl
29	480	65.1	119	7	US-11-097-812-74	Sequence 74, Appl
30	480	65.1	119	7	US-11-097-812-76	Sequence 76, Appl
31	480	65.1	119	7	US-11-097-812-81	Sequence 81, Appl
32	480	65.1	136	7	US-11-250-411-95	Sequence 95, Appl
33	479	65.0	120	7	US-11-097-812-144	Sequence 144, App
34	479	64.9	478	7	US-11-193-512-78	Sequence 78, Appl
35	477	64.7	462	7	US-11-177-648-30	Sequence 30, Appl
36	476.5	64.7	477	7	US-11-037-199-5	Sequence 5, Appll
37	474.5	64.4	130	7	US-11-097-820-6	Sequence 6, Appll
38	473	64.2	119	7	US-11-097-812-63	Sequence 63, Appl
39	473	64.2	119	7	US-11-097-812-64	Sequence 64, Appl
40	473	64.2	119	7	US-11-097-812-65	Sequence 65, Appl
41	473	64.2	119	7	US-11-097-812-70	Sequence 70, Appl
42	473	64.2	119	7	US-11-097-812-75	Sequence 75, Appl
43	473	64.2	119	7	US-11-097-812-77	Sequence 77, Appl
44	473	64.2	119	7	US-11-097-812-80	Sequence 80, Appl
45	473	64.2	119	7	US-11-097-812-206	Sequence 206, App

ALIGNMENTS

RESULT 1
US-11-165-023-16
Sequence 16, Application No. US2006019342A1
Publication No. US2006019342A1
GENERAL INFORMATION:
; APPLICANT: Dall'Acqua, William
; APPLICANT: Wu, Herren
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: INCREASING THE PRODUCTION OF RECOMBINANT ANTIBODIES IN MAMMALIAN
; TITLE OF INVENTION: CELLS BY SITE-DIRECTED MUTAGENESIS
; FILE REFERENCE: AE700US
; CURRENT APPLICATION NUMBER: US/11/165,023
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: US 60/583,184
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/624,153
; PRIOR FILING DATE: 2004-11-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin version 3.3
;
; SEQ ID NO 16
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: recombinant antibody variable region
US-11-165-023-16

Query Match   77.5%; Score 571; DB 7; Length 115;
Best Local Similarity   92.3%; Pred. No. 1e-39;
Matches 108; Conservative   3; Mismatches   4; Indels   2; Gaps   1;

Qy   20 EVQLQQSGPELVKTGASVKISCKASGYSFTGYTMHWVKQSHGKSLEWIGYISCYNGATSY 79
         ||||||||||||||||||||||||||||||||||||||||||||:||||||||||:||
Db   1 EVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGYISCYNGVTSY 60

Qy   80 NQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGANWVFDYWGQGTTLTVSS 136
         |||||||||||||||||||| ||||||||||||||||||| ::|||||||||:|||
Db   61 NQKFKGKATFTVDTSSSTAYMQNSLTSEDSAVYYCAR--SHAMDYWGQGTSVTVSS 115

RESULT 2
US-11-074-373-39
; Sequence 39, Application US/11074373
; Publication No. US2006024302A1
; GENERAL INFORMATION:
; APPLICANT: Achen et al.
; TITLE OF INVENTION: CHIMERIC ANTI-VEGF-D ANTIBODIES AND HUMANIZED ANTI-VEGF-D ANTIBOD
; TITLE OF INVENTION: AND METHODS OF USING SAME

; FILE REFERENCE: 28967/39969A
; CURRENT APPLICATION NUMBER: US/11/074,373
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 39
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-074-373-39

Query Match   77.3%;   Score 569.5; DB 7; Length 137;
Best Local Similarity   78.1%;   Pred. No. 1.6e-39;
Matches 107; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

Qy   1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH 60
         ||| | |||||||: || ||:|||||||||| ||||| ||||||||||||| |:|||||
Db   1 MGWSGVFLFLLSGSTGVHSEIQLQQSGPELVKPGASVKVSCKASGYSFTGYNMYWVKQSH 60

Qy   61 GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGAN 120
         ||||||||| :|||| |||||||||||:||| ||||||: |:||||||||||||||
Db   61 GKSLEWIGYIDPYNGDTTYNQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARTSY 120

Qy 121 W-VFDYWGQGTTLTVSS 136
         : :.|||||||::.|||
Db 121 YGGMDYWGQGTSVTVSS 137

RESULT 3
US-11-165-023-31
Sequence 31, Application US/11165023
Publication No. US20060019342A1
GENERAL INFORMATION:
; APPLICANT: Dall'Acqua, William
; APPLICANT: Wu, Herren
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: INCREASING THE PRODUCTION OF RECOMBINANT ANTIBODIES IN MAMMALIAN
; TITLE OF INVENTION: CELLS BY SITE-DIRECTED MUTAGENESIS
; FILE REFERENCE: AE700US
; CURRENT APPLICATION NUMBER: US/11/165,023
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: US 60/583,184
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/624,153
; PRIOR FILING DATE: 2004-11-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin version 3.3
;
; SEQ ID NO 31
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: recombinant antibody variable region
US-11-165-023-31

Query Match   90.6%;   Score 558; DB 7; Length 115;
Best Local Similarity   90.6%;   Pred. No. 1.1e-38;
Matches 106; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

Qy   20 EVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGYISCYNGATSY 79
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   1 EVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGYISCYNGVTSY 60

Qy   80 NQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGANWFDYWGQGTTLTVSS 136
         | |||||||||||||||||||||||||||||||||||| ||: ||||||| |||||
Db   61 ADKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCAR--SHAMDYWGQGTSVTVSS 115

RESULT 4
US-11-165-023-32
Sequence 32, Application US/11165023
Publication No. US20060019342A1
GENERAL INFORMATION:

Query Match   75.7%;   Score 541.5; DB 7; Length 115;
Best Local Similarity   90.6%;   Pred. No. 1.1e-38;
Matches 106; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

Qy   20 EVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGYISCYNGATSY 79
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   1 EVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGYISCYNGVTSY 60

Qy   80 NQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGANWFDYWGQGTTLTVSS 136
         | |||||||||||||||||||||||||||||||||||| ||: ||||||| |||||
Db   61 ADKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCAR--SHAMDYWGQGTSVTVSS 115

; APPLICANT: Dall'Acqua, William
; APPLICANT: Wu, Herren
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: INCREASING THE PRODUCTION OF RECOMBINANT ANTIBODIES IN MAMMALIAN
; TITLE OF INVENTION: CELLS BY SITE-DIRECTED MUTAGENESIS
; FILE REFERENCE: AE700US
; CURRENT APPLICATION NUMBER: US/11/165,023
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: US 60/583,184
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/624,153
; PRIOR FILING DATE: 2004-11-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin version 3.3
;
; SEQ ID NO 32
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: recombinant antibody variable region
US-11-165-023-32

RESULT 5
US-10-016-686-4
Sequence 4, Application US/10016686
Publication No. US20060142222A1
GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: Kingsman, Alan
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Bebbington, Christopher Robert
; APPLICANT: Carrol, Miles William
; APPLICANT: Ellard, Fiona Margaret
; APPLICANT: Myers, Kevin Alan
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 674523-2012
; CURRENT APPLICATION NUMBER: US/10/016,686
; CURRENT FILING DATE: 2002-11-02
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 4
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deduced amino acid sequence for the Ig-574 fusion protein
US-10-016-686-4

Query Match   73.5%;   Score 541.5; DB 6; Length 592;
Best Local Similarity   75.5%;   Pred. No. 1e-36;
Matches 105; Conservative 9; Mismatches 22; Indels 3; Gaps 1;

Qy   1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH 60
         ||| | ||:: :|:| ||||||||||||||| ||||||||||||||||||||||||||
Db   1 MGWSCIILFLVATATGVHSEVQLQQSGPELVKPGASVKISCKASGYSFTGYYMHWVKQSH 60

Qy   61 GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARG-- 118
         |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARG-- 118

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: March 21, 2006, 17:50:10 ; Search time 301.766 Seconds
                (without alignments)
                198.019 Million cell updates/sec

Title: US-10-768-193-7
Perfect Score: 737
Sequence: 1 MGWIWIFLFLLSGTRAGVHSE.........RGANWVFDYWGQGTTLTVSS 136

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 43937878l residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
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                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003aa:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*
                9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	737	100.0	136	6	ABU08927	Abu08927 Mouse amy
2	640.9	86.9	137	6	ADS94331	Ads94331 Antibody
3	594.5	80.7	135	2	AAR05090	Aar05090 Heavy cha
4	594.5	80.7	135	3	AAW60866	Aaw60866 Variable
5	594.5	80.7	590	2	AAY80293	Aay80293 IgM chime
6	594.5	80.7	590	2	AAW31751	Aaw31751 H chain s
7	594.5	80.7	590	3	AAW71888	Aaw71888 Anti-huma
8	593.5	80.7	590	3	AAB12908	Aab12908 Anti-huma
9	593.5	80.5	135	4	AAW68548	Aaw68548 Anti-CD33
10	593.5	80.5	135	2	AAB69682	Aab69682 Murine M1
11	590.5	80.5	135	8	AAR28669	Aar28669 p12-h2. 3
12	590.5	80.1	135	2	ADS94335	Ads94335 Antibody
13	585.5	79.4	139	8	ADR73595	Adr73595 Anti-AR a
14	581	78.8	138	8	AAR05090	Aar05090 Heavy cha
15	575.5	78.1	137	2	AAE38408	Aae38408 Mouse vir
16	575.5	78.1	467	6	AAW03724	Aaw03724 Anti-huma
17	573.5	77.8	137	2	AEA34944	Aea34944 Human ant
18	571	77.5	115	9	AEB17185	Aeb17185 EphA2-spe
19	571	77.5	115	9	AEA42985	Aea42985 EphA2 ant
20	571	77.5	115	9	ADJ57084	Adj57084 3G4 antib
21	567.5	77.0	159	8	ADJ57088	Adj57088 3G4-
22	567.5	77.0	152	8	AAB69688	Aab69688 Murine CM
23	564	76.5	138	4	ADO47789	Ado47789 Mouse CMV
24	562.5	76.3	133	8	ADO00820	Ado00820 Antibody
25	562.5	76.3	133	8	ADO43850	Ado43850 Heavy cha
26	562.5	76.3	133	8	ADO43846	Ado43846 Heavy cha
27	562.5	76.3	133	9	ADZ08854	Adz08854 Mammalian
28	562	76.3	140	2	AAW06213	Aaw06213 MAb Co-1
29	562	76.3	140	2	AAW85061	Aaw85061 Mouse Co-
30	562	76.3	140	6	ABU58895	Abu58895 Mouse ant
31	562	76.3	438	5	AAE18372	Aae18372 Human pen
32	562	76.3	438	5	ABG76347	Abg76347 Portion o
33	562	76.3	456	5	AAE18370	Aae18370 Human pen
34	562	76.3	456	5	ABG76345	Abg76345 Mouse DAV
35	562	76.3	456	9	AEB96754	Aeb96754 DAV-1 ant
36	562	76.3	493	5	AAE18379	Aae18379 Human N-t
37	562	76.3	493	5	ABG76354	Abg76354 Mouse DAV
38	562	76.3	510	5	AAE18378	Aae18378 Human N-t
39	562	76.3	510	5	ABG76353	Abg76353 Mouse DAV
40	562	76.3	597	5	AAE18377	Aae18377 Human N-t
41	562	76.3	597	5	ABG76352	Abg76352 Mouse DAV
42	562	76.3	613	5	AAE18380	Aae18380 Human N-t
43	562	76.3	613	5	ABG76355	Abg76355 Mouse DAV
44	557.5	75.6	215	3	AAU78254	Aau78254 Mouse agg
45	557	75.6	132	2	AAW03183	Aaw03183 Guy's 13

ALIGNMENTS

RESULT 1
ID   ABU08927 standard; protein; 136 AA.
AC   ABU08927;
DT   03-JUN-2003 (first entry)
DE   Mouse amyloid beta antibody heavy chain variable region.
KW   Mouse; antibody; beta-amyloid fibril inhibitor; Alzheimer's disease;
KW   GM1 ganglioside-bound amyloid beta protein; amyloid beta protein;
KW   amyloid fibril formation inhibition; heavy chain; variable region.
OS   Mus musculus.

FH   Key   Location/Qualifiers
FH
FT   Peptide   1..19
FT   /label= Signal_sequence
FT   Protein   20..136
FT   /note= "Mature GM1 ganglioside-bound amyloid beta
FT   antibody heavy chain variable region."
FT   Region   50..54
FT   /label= CDR1
FT   /note= "Complementarity determining region 1.
FT   Specifically claimed in claim 1"
FT   Region   69..85
FT   /label= CDR2
FT   /note= "Complementarity determining region 2.
FT   Specifically claimed in claim 1"
FT   Region   118..125
FT   /label= CDR3
FT   /note= "Complementarity determining region 3.
FT   Specifically claimed in claim 1"

PN   WO200301462-A1.
PD   20-FEB-2003.
PF   01-AUG-2002; 2002WO-JP007874.
PR   03-AUG-2001; 2001JP-00235700.
PA   (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
PA   (NICH-) JAPAN CHUBU NAT HOSPITAL.
PA   (YANA/) YANAGISAWA K.

PI Yanagisawa K, Shibata M;
XX
DR WPI; 2003-268182/26.
DR N-PSDB; ABX93688.
XX
PT Antibodies recognising GM1 ganglioside-bound amyloid beta-protein and
PT encoded DNAs, useful in diagnosing, preventing or treating Alzheimer's
PT disease by inhibiting early-stage beta-amyloid fibril formation.
XX
PS Claim 4; Fig 1; 60pp; Japanese.
XX
CC The invention relates to four antibodies recognising GM1 ganglioside-
CC bound amyloid beta protein and having inhibitory activity on the
CC formation of amyloid fibril. The antibodies are useful in diagnosing,
CC preventing or treating Alzheimer's disease by inhibiting early-stage,
CC amyloid fibril formation. The antibody does not recognise soluble
CC antigen-binding amyloid beta-protein, and thus drugs produced from the antibodies are
CC efficacious in treating Alzheimer's disease. The present sequence
CC represents the amino acid sequence of mouse-GM1 ganglioside-bound amyloid
CC beta antibody heavy chain variable region
XX
SQ Sequence 136 AA;

Query Match   100.0%; Score 737; DB 6; Length 136;
Best Local Similarity 100.0%;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1  MGWIWIFLFLLSGTRAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH  60
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Db   1  MGWIWIFLFLLSGTRAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH  60

Qy  61  GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGAN 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61  GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGAN 120

Qy 121  WVFDYWGQGTTLTVSS 136
        ||||||||||||||||
Db 121  WVFDYWGQGTTLTVSS 136
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RESULT 2

AC ADS94331;
ID ADS94331 standard; protein; 137 AA.
XX
DT 02-DEC-2004 (first entry)
XX
DE Antibody 368.1 heavy chain variable region (368.1H) SEQ ID NO:30.
XX
KW antibody; antigen-binding antibody fragment;
KW cell-associated CA 125/O772P; monoclonal antibody; cytostatic;
KW immunostimulant; mediator of lysis; tumour; cell proliferative disorder;
KW cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;
KW ovarian cancer.
OS Synthetic.
XX
PN WO2004035537-A2.
XX
PD 29-APR-2004.
XX
PF 15-OCT-2003; 2003WO-US032945.
PR 16-OCT-2002; 2002US-0418828P.
PR 10-JUL-2003; 2003US-0485986P.
XX
PA (EURO-) EUROCELTIQUE SA.
XX
PI Albone EF, Soltis DA;
XX
DR WPI; 2004-357171/33.
DR N-PSDB; ADS94339.
XX
PT Novel isolated antibody, or antigen-binding antibody fragment binding
PT with cell-associated CA 125/O772P polypeptide relative to shed CA
PT 125/O772 polypeptide, useful for ameliorating cervical or ovarian cancer.
XX
PS Claim 36; SEQ ID NO 30; 153pp; English.
XX
CC The present invention describes an isolated antibody, or an antigen-
CC binding antibody fragment (I), that preferentially binds cell-associated
CC CA 125/O772P polypeptide relative to shed CA 125/O772 polypeptide. Also
CC described: (1) a monoclonal antibody that competes with binding of (II); (3) a hybridoma
CC as deposited in (III); (4) an isolated nucleic acid molecule (III)
CC comprising a nucleotide sequence that encodes a variable chain region of
CC (I); (5) a pharmaceutical composition comprising an antibody or an
CC antigen-binding antibody fragment that preferentially binds cell-
CC associated CA 125/O772P polypeptide relative to shed CA 125/O772P
CC polypeptide, and a carrier; (6) a pharmaceutical composition comprising a
CC monoclonal antibody or an antigen-binding monoclonal antibody fragment
CC that preferentially binds cell-associated CA 125/O772P polypeptide
CC relative to shed CA 125/O772P polypeptide, and a carrier; (7) an article
CC of manufacture (IV) comprising packaging material and a composition
CC comprising an antibody, or an antigen-binding antibody fragment that
CC preferentially binds cell-associated CA 125/O772P relative to shed CA
CC 125/O772P, and a carrier contained within the packaging material, and
CC composition in a form suitable for administration to a subject; (8) a
CC fusion polypeptide (V) comprising an antibody, or an antigen-binding
CC antibody fragment, which preferentially binds cell-associated CA
CC 125/O772P relative to shed CA 125/O772P operably linked to a heterologous
CC agent; (9) ameliorating (M1) a symptom of a CA 125/O772P-related disorder
CC ; (10) a monoclonal antibody (VI) chosen from 325.1, 621.1, 633.1, 654.1,
CC 725.1, 8G9, 7F10, 8A1, 8AC3, 15C9, 8E3, 8B5, 7G10, 16C7, 7C6, 7H1, 16H9,
CC 7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding
CC antibody fragment; (11) an antigen binding antibody fragment
CC that competes with (VI); and (12) a pharmaceutical composition comprising
CC (VI) and a carrier. (I) has cytostatic activity, and can be used as an
CC immunostimulant and a mediator of lysis of positive tumour cell. (I) is
CC useful for ameliorating a symptom of a CA 125/O772-related disorder which
CC is a cell proliferative disorder such as cancer, cervical or uterine
CC cancer, breast or lung cancer or ovarian cancer. (V) is useful
CC diagnostically for monitoring the development or progression of cancer or
CC tumour as part of clinical testing procedure. The present sequence
CC represents an antibody heavy chain variable region amino acid sequence,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 137 AA;

Query Match   86.9%; Score 640.5; DB 8; Length 137;
Best Local Similarity 87.6%; Pred. No. 2.8e-44;
Matches 120; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

```
Qy   1  MGWIWIFLFLLSGTRAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH  60
        |||||||||||||| ||||||||||||||| |||||||||||||||||| ||||||||| 
Db   1  MGWIWIFLFLLSGT-AGVHSEVQLQQSGPELVRTGASVKISCKASGYSFTGRYMHWVKQSL  60

Qy  61  GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCAR-GA 119
        |||||||| ||||||||||||||||||||||||||||| |||||||||||||||| |
Db  61  GKSLEWIGYVSCYNGATSYNQKFKGKATFTVDTSSSTAYMQLNSLTSEDSAVYYCAREGD 120

Qy 120  NWVFDYWGQGTTLTVSS 136
        :  :| ||||| |||||
Db 121  YYSMDFWGQGTSVTVSS 137
```

RESULT 3

AC AAW60866;
ID AAW60866 standard; protein; 135 AA.
XX
DT 10-SEP-1998 (first entry)
XX
DE Variable region of an anti-Fas antibody heavy chain.

OM protein - protein search, using sw model

GenCore version 5.1.7
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Run on: March 21, 2006, 18:00:46 ; Search time 25.1472 Seconds
(without alignments)
520.356 Million cell updates/sec

Title: US-10-768-193-7
Perfect Score: 737
Sequence: 1 MGWIWIFLFLLSGTAGVHSE..........RGANWVFDYWGQGTTLTVSS 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	596	80.9	140	2	T01407	Ig heavy chain (my
2	592.5	80.4	137	2	H32513	Ig heavy chain pre
3	583.	79.2	139	2	A27609	Ig heavy chain pre
4	561.5	76.2	135	2	PS0057	Ig heavy chain pre
5	558	75.7	138	2	PH0105	Ig heavy chain pre
6	540.5	73.3	469	1	S37483	anti-digoxin trans
7	540	73.3	117	2	S37483	Ig gamma-2a chain
8	532	72.2	140	2	PH1482	Ig heavy chain pre
9	532	72.2	117	2	HVMS8A	Ig heavy chain V r
10	527	71.5	138	2	S45249	Ig heavy chain pre
11	527	71.5	151	2	PL0011	Ig heavy chain pre
12	522	70.8	140	2	PH1489	Ig heavy chain V r
13	521	70.7	166	2	PL0012	Ig heavy chain pre
14	519	70.4	140	2	HVMSG7	Ig heavy chain pre
15	514.5	69.8	150	2	PN0444	Ig heavy chain pre
16	514	69.7	136	1	HVMSB1	Ig heavy chain V r
17	511.5	69.4	474	2	G2MS11	Ig gamma-2b chain
18	510	69.2	140	2	PH1488	Ig heavy chain V r
19	507	68.8	117	2	MHMS4E	Ig heavy chain V r
20	507	68.8	135	2	MHMSJ5	Ig heavy chain V r
21	505	68.5	135	2	PH1493	Ig heavy chain V r
22	505	68.5	140	2	PH1484	Ig heavy chain V r
23	504	68.4	135	2	PH1492	Ig heavy chain V r
24	501.5	68.0	112	2	S09957	Ig heavy chain V-D
25	501	68.0	138	2	S21810	Ig heavy chain V r
26	501	68.0	140	2	A36194	Ig heavy chain V r
27	500	67.8	140	1	PH1498	Ig heavy chain pre
28	499.5	67.8	139	1	MHMS18	Ig heavy chain V r
29	498.5	67.6	119	2	F30502	Ig heavy chain pre
29	495.5	67.2	139	2	PS0024	Ig heavy chain pre
30	493	66.9	140	2	PH1486	Ig heavy chain V r
31	491	66.6	140	2	PH1483	Ig heavy chain V r
32	491	66.6	136	2	PL0208	Ig heavy chain pre
33	488.5	66.3	141	2	JL0076	Ig heavy chain V r
34	487.5	66.1	128	2	I37267	Ig heavy chain V r
35	481.5	65.3	120	2	A49982	Ig heavy chain V r
36	481.5	65.3	133	2	PC1155	Ig heavy chain pre
37	480.5	65.2	122	2	PC1155	Ig heavy chain pre
38	479.5	65.1	118	1	PH0887	Ig heavy chain V r
39	479	65.0	135	2	PH1494	Ig heavy chain pre
40	478	64.9	138	2	MHMS38	Ig heavy chain V r
41	475	64.4	141	2	A39276	anti-DNA autoantib
42	474.5	64.4	135	1	PL0200	Ig heavy chain pre
43	473.5	64.2	137	2	E32513	Ig heavy chain pre
44	472	64.0	137	1	G2MS43	Ig gamma chain - m
45	472	64.0	446	2	S40295	Ig gamma-2a chain

ALIGNMENTS

RESULT 1
T01407
Ig heavy chain (myeloma M104E) - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C;Accession: T01407
R;Takahashi, S.; Matsuura, Y.; Taniguchi, T.; Tamura, H.; Bitoh, S.; Onishi, S.; Yamamot
A;Title:Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and
Microbiol. Immunol. 36, 855-863, 1992
A;Reference number: Z14317; MUID:93116638; PMID:1474935
A;Accession: T01407
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-140 <TAK>
A;Cross-references: UNIPARC:UPI000011B29E; EMBL:S51851; NID:g262657
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 80.9%; Score 596; DB 2; Length 140;
Best Local Similarity 83.8%; Pred. No. 1.3e-43;
Matches 114; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

```
Qy   1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKICKASGYSFTGYYMHWVKQSH 60
         |||| |||||||||||| |||||||||||||| ||||| |||||||| ||| |||||
Db   1 MGWSWIFLFLLSGTAGVLSEVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSH 60

Qy  61 GKSLEWIGYISCYNGATSYNQKFKGKATFVDTSSSTAYMQFNSLTSEDSAVYYCARGAN 120
         |||||||  :  ||||||||||||||  |||   |||||| ||||||||||||||| :
Db  61 GKSLEWIGDINPNNGGTSYNQKFKGKATLIVDKSSSTAYMQLNSLTSEDSAVYYCARDYD 120

Qy 121 WVFDYWGQGTTLTVSS 136
        | ||  || |||||||
Db 121 WYFDVWGAGTTVTVSS 136
```

RESULT 2
H32513
Ig heavy chain precursor V region (BXW16) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: H32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: H32513
A;Molecule type: DNA
A;Residues: 1-137 <KOF>
A;Cross-references: UNIPARC:UPI00000114D9A; GB:M20831; NID:g196949; PIDN:AAA38848.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMW>

RESULT 3
A27609
Ig heavy chain precursor V region (I29) - mouse

```
Query Match             84.2%;
Best Local Similarity   80.4%;  Score 592.5;  DB 2;  Length 137;
Matches  117;  Conservative   6;  Mismatches  11;  Indels   5;  Gaps   2;

Qy    1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH  60
        |||| ||||||| |||||||  ||||| ||| |||||||||||||||||||| : |||||
Db    1 MGWSWIFLFLLSVTAGVHSEIQLQQSGAELVRPGASVKISCKASGYSFTGYNMNWVKQSH  60

Qy   61 GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCAR---  117
        ||||||| |   : ||||||||||||| ||| |||||||| |||||||||||||||
Db   61 GKSLEWIGNINPYGSTSYNQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARKNY  120

Qy  118 GANWVFDYWGQGTTLTVSS  136
        |  ||||||||||||||
Db  121 GSS--FDYWGQGTTLTVSS  137
```

C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: A27609
R;Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J;Immunol. 140, 1676-1684, 1988
A;Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain swit...
A;Reference number: A27609; MUID:88154467; PMID:3126234
A;Accession: A27609
A;Molecule type: DNA
A;Residues: 1-139 <KLE>
A;Cross-references: UNIPARC:UPI000011AD5D; EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PI...
A;Genetic:
A;Introns: 16/1
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-135/Product: Ig heavy chain V region PAR #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

RESULT 4
PS0057
Ig heavy chain precursor V region (PAR) - mouse

```
Query Match             81.3%;
Best Local Similarity   79.2%;  Score 583.5;  DB 2;  Length 139;
Matches  113;  Conservative   9;  Mismatches  14;  Indels   3;  Gaps   1;

Qy    1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH  60
        |||| |||||| |||||||||||||||||||||||||
Db    1 MGWSWIFLFLLSGTAGVLSEVQLQQSGPELVKGASVHSEIQLQQSGPELVKPGASVKMSCKASGYTFTDYVMHWVKQSH  60

Qy   61 GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGAN  120
        ||||||| |   |  ||||||||||| ||| |||||||| |||||||||||||||
Db   61 GKSLEWIGYINPYDYTSYNQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARYSY  120

Qy  121 WVF---DYWGQGTTLTVSS  136
        || :  |||| ||| |||
Db  121 YSYYAMDYWGGGTSVTVSS  139
```

C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
C;Accession: PS0057
R;Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
J;Biochem. 104, 337-343, 1988
A;Title: Biased expression of variable region gene families of the immunoglobulin heavy
A;Reference number: PS0057; MUID:89197817; PMID:2467902
A;Accession: PS0057
A;Molecule type: DNA
A;Residues: 1-135 <YAO>
A;Cross-references: UNIPARC:UPI000011B257; GB:D00307; NID:g220448; PID:BAA00213.1; PID:...
A;Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly
A;Comment: The gene encoding this protein was isolated from a hybridoma that produces an
C;Superfamily: immunoglobulin V region; immunoglobulin homology

RESULT 5
PH0105
anti-digoxin transfectoma antibody light chain V region precursor - mouse (fragment)

```
Query Match             76.2%;
Best Local Similarity   80.9%;  Score 561.5;  DB 2;  Length 110;
Matches  110;  Conservative   8;  Mismatches  17;  Indels   1;  Gaps   1;

Qy    1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH  60
        |||| ||||||||||||| ||||||||||||| |||| :||| ||| |||: : ||:| :
Db    1 MGWSWIFLFLLSGTAGVLSEVQLQQSGPELVKPGASVRMSCKSSGYIFTDYMMNWVRQSN  60

Qy   61 GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGAN  120
        |||||||| ||| ::  ||||||||||| ||| |||| : : ||||||||||||||  :
Db   61 GKSLEWIGRINPYNGDTFYNQKFKGKATLTVDKSSSTAHMELRSLTSEDSAVYYCAR-LN  119

Qy  121 WVFDYWGQGTTLTVSS  136
        | : |||: |||||
Db  120 YRGAYWQGTLVTVSA  135
```

C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: PH0105
R;Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.
Mol. Immunol. 27, 901-909, 1990
A;Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain
A;Reference number: PH0105
A;Molecule type: mRNA
A;Residues: 1-138 <NEA>
A;Status: preliminary
A;Accession: PH0105
A;Cross-references: UNIPARC:UPI000011SEC4; GB:X56622; GB:S44836; NID:g9875; PIDN:CAA399...
A;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

RESULT 6
S37483
Ig gamma-2a chain - mouse

```
Query Match             75.7%;
Best Local Similarity   76.1%;  Score 558;  DB 2;  Length 138;
Matches  105;  Conservative  12;  Mismatches  19;  Indels   2;  Gaps   2;

Qy    1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH  60
        |||| |||||||||||| ||||||||||||| |||| :||| ||| |||: : ||:| :
Db    1 MGWSWIFLFLLSGTAGVLSEVQLQQSGPELVKPGASVRMSCKSSGYIFTDYMMNWVRQSN  60

Qy   61 GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCAGSSG  120
        ||||  || |  | ||  :||||||||| ||| |||||| : ||||||||||||||  :
Db   61 GKSLDVIGYISPYSGVTGYKNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAGSSG  120

Qy  119 ANWVFDYWGQGTTLTVSS  136
        | || ||||  |: ||
Db  121 NKWAMDYWGHGASVTVSS  138
```

C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.
A;submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-469 <DUC>
A;Cross-references: UNIPARC:UPI00002F847; EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PII...
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin

OM protein - protein search, using sw model

GenCore version 5.1.7
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Run on: March 21, 2006, 17:50:40 ; Search time 151.396 Seconds
(without alignments)
633.780 Million cell updates/sec

Title: US-10-768-193-7
Perfect score: 737
Sequence: 1 MGWIWIFLFLLSGTAGVHSE.......RGANWVFDYWGQGTTLTVSS 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	605	82.1	470	2	Q7TMK1_MOUSE	q7tmk1 mus musculu
2	592	80.3	472	2	Q6PJA7_MOUSE	q6pja7 mus musculu
3	586	79.5	483	2	Q4VAB6_MOUSE	q4vab6 mus musculu
4	567.5	77.0	488	2	Q91WR1_MOUSE	q91wr1 mus musculu
5	548	74.4	477	2	Q58E56_MOUSE	q58e56 mus musculu
6	546	74.1	481	2	Q91WT1_MOUSE	q91wt1 mus musculu
7	542.5	73.6	481	2	Q8VCV5_MOUSE	q8vcv5 mus musculu
8	540	73.3	117	1	HV14_MOUSE	p01758 mus musculu
9	539.5	73.2	465	2	Q6PJB2_MOUSE	q6pjb2 mus musculu
10	539	73.1	118	2	Q5R3X0_MOUSE	q5r3x0 mus musculu
11	519	70.4	140	1	HV02_MOUSE	p01746 mus musculu
12	516.5	70.1	613	2	Q8VCX7_MOUSE	q8vcx7 mus musculu
13	516	70.0	117	2	Q9QXF0_MOUSE	q9qxf0 mus musculu
14	514	69.7	134	2	Q652R6_MOUSE	q652r6 mus musculu
15	514	69.7	136	2	Q59W9_MOUSE	q59w9 mus musculu
16	510	69.2	168	2	Q8VDC9_MOUSE	q8vdc9 mus musculu
17	509	69.1	168	1	HV15_MOUSE	p01759 mus musculu
18	507	68.8	117	1	HV12_MOUSE	p01756 mus musculu
19	505	68.5	117	1	HV13_MOUSE	p01757 mus musculu
20	502	68.1	475	2	Q5FVP3_RAT	q5fvp3 rattus norv
21	501	68.0	117	2	Q9QXE9_MOUSE	q9qxe9 mus musculu
22	499.5	67.8	139	1	HV07_MOUSE	p01751 mus musculu
23	499	67.7	473	2	Q9D8L4_MOUSE	q9d8l4 mus musculu
24	496.5	67.7	590	2	Q4V9V8_MOUSE	q4v9v8 mus musculu
25	496.5	67.4	617	2	Q4KML5_MOUSE	q4kml5 mus musculu
26	494.5	67.1	485	2	Q58E61_MOUSE	q58e61 mus musculu
27	491.5	66.7	463	2	Q99LC4_MOUSE	q99lc4 mus musculu
28	491	66.6	480	2	Q8K0Z4_MOUSE	q8k0z4 mus musculu
29	488	66.2	464	2	Q6PF95_MOUSE	q6pf95 mus musculu
30	488	66.2	464	2	Q7TMT6_MOUSE	q7tmt6 mus musculu
31	485.5	65.9	482	2	Q8K172_MOUSE	q8k172 mus musculu
32	484.5	65.7	591	2	Q4QGW0_RAT	q4qgw0 rattus norv
33	480	65.1	616	2	Q504M7_MOUSE	q504m7 mus musculu
34	479.5	65.1	118	1	HV51_MOUSE	p06330 mus musculu
35	479	65.0	458	2	Q5BK05_RAT	q5bk05 rattus norv
36	477.5	64.8	598	2	Q568Y0_RAT	q568y0 rattus norv
37	475	64.8	458	2	Q5B2Z2_RAT	q5b2z2 rattus norv
38	473.5	64.2	137	1	HV11_MOUSE	p01755 mus musculu
39	473	64.2	137	2	Q52L51_MOUSE	q52l51 mus musculu
40	470.5	63.8	489	1	HV52_MOUSE	p06327 mus musculu
41	467	63.4	487	2	Q8VCX4_MOUSE	q8vcx4 mus musculu
42	464	63.0	483	2	Q52L2_9MURI	q52l2 mus sp. fv/
43	463	62.8	117	2	Q920E8_MOUSE	q920e8 mus musculu
44	461.5	62.6	120	2	Q8K0F2_MOUSE	q8k0f2 mus musculu
45	458.5	62.2	486	2	Q5H2Y6_MOUSE	q5h2y6 mus musculu

ALIGNMENTS

RESULT 1
Q7TMK1_MOUSE

```
ID   Q7TMK1_MOUSE PRELIMINARY;        PRT;   470 AA.
AC   Q7TMK1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein AI324046.
GN   Name=AI324046;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RA   Expression driven by an MMTV-LTR enhancer.;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055910; AAH55910.1; -; mRNA.
DR   HSSP; P01865; 1KB5.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
```

```
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW   Hypothetical protein; Immunoglobulin domain.
SQ   SEQUENCE   470 AA;  51728 MW;  6D90B4DF896BB090 CRC64;

Query Match             82.1%;  Score 605;  DB 2;  Length 470;
Best Local Similarity   82.1%;
Matches  115;  Conservative    7;  Mismatches   14;  Indels    4;  Gaps    1;

Qy    1 MGWIWIFLFLLSGTPGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH 60
          ||| | ||||||||| || |||||||||||||| |||||||||||||| ||||||||||
Db    1 MGWSWVFLFLLSGTAGVLSEVQLQQSGPELVKPGASVKISCKASGYTFTGYYMHWVKQSH 60

Qy   61 GKSLEWIGYISCYNGAISYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCAR--- 117
          |||||||| |   || :||||||||||| |||:||||||| :|||||||||||||
Db   61 GKSLEWIGLVNPSNGDTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYYCARYY 120

Qy  118 -GANWVFDYWGQGTTLTVSS 136
          :|:||:||||||||:||||
Db  121 SGSYWYFDVWGAGTTVTVSS 140
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RESULT 2
Q6PJA7_MOUSE

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ID   Q6PJA7_MOUSE PRELIMINARY;      PRT;    472 AA.
AC   Q6PJA7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
GN   Name=Igh-1a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
```

RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018535; AAH18535.1; -; mRNA.
DR   HSSP; P01865; 1KB5.

```
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW   Hypothetical protein; Immunoglobulin domain.
SQ   SEQUENCE   472 AA;  52299 MW;  16516GC23D55D4AB CRC64;

Query Match             80.3%;  Score 592;  DB 2;  Length 472;
Best Local Similarity   80.3%;
Matches  114;  Conservative    6;  Mismatches   16;  Indels    6;  Gaps    1;

Qy    1 MGWIWIFLFLLSGTPGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH 60
          ||| | ||||||||| || |||||||||||||| |||||||||||||| ||||||||||
Db    1 MGWSWIFLFLLSGTAGVLSEVQLQQSGPELVKPGASVKISCKASGYTFTGYYMHWVKQSH 60

Qy   61 GKSLEWIGYISCYNGAISYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARG-- 118
          |||||||| |   || :||||||||||: ||||:||||||| ||| ||||||||||||
Db   61 GKSLEWIGYIYPNNGGNGYNQKFKGKAILTVDKSSSTAYMELRSLTSEDSAVYFSDYYMHWVKQSH 120

Qy  119 ----ANWVFDYWGQGTTLTVSS 136
          ||||| |||||||:||||
Db  121 SYYSYDHYFDYWGGGTTVTVSS 142
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RESULT 3
Q4VAB6_MOUSE

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ID   Q4VAB6_MOUSE PRELIMINARY;      PRT;    483 AA.
AC   Q4VAB6;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   Name=Igh-1a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
```

RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;

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DR   MGI; MGI:96443; Igh-1a.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW   Hypothetical protein.
```

OM protein - protein search, using sw model

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GenCore version 5.1.7

Run on: March 21, 2006, 18:06:30 ; Search time 122.657 Seconds
                 (without alignments)
                 463.284 Million cell updates/sec

Title: US-10-768-193-7 .
Perfect Score: 737
Sequence: 1 MGWIWIFLFLLSGTAGVHSE.........RGANWFDYWGQGTTLTVSS 136
Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA Main:*
                 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	DB ID	Description
1	737	100.0	136	4	US-10-768-193-7	Sequence 7, Appli
2	640.5	86.9	137	5	US-10-687-035-30	Sequence 30, Appli
3	601.5	81.6	137	4	US-10-462-062-153	Sequence 153, App
4	601.5	81.6	137	4	US-10-462-062-154	Sequence 154, App
5	593.5	80.5	135	4	US-10-389-155-60	Sequence 60, Appl
6	593.5	80.5	135	4	US-10-389-417-60	Sequence 60, Appl
7	593.5	80.5	135	4	US-10-452-357-69	Sequence 69, Appl
8	593.5	80.5	135	5	US-10-837-904-27	Sequence 27, Appl
9	585.5	79.4	139	5	US-10-687-035-34	Sequence 34, Appl
10	581	78.8	138	4	US-10-774-776-9	Sequence 9, Appli
11	575.5	78.1	467	5	US-10-500-696-2	Sequence 2, Appli
12	571	77.5	115	5	US-10-994-129-21	Sequence 21, Appl
13	571	77.5	115	6	US-11-004-795A-53	Sequence 53, Appl
14	571	77.5	115	4	US-11-004-794A-53	Sequence 53, App
15	567.5	77.0	152	4	US-10-642-120-2	Sequence 2, Appl
16	567.5	77.0	152	4	US-10-642-060-2	Sequence 2, Appl
17	567.5	77.0	152	4	US-10-687-035-2	Sequence 2, Appli
18	567.5	77.0	152	4	US-10-642-059-2	Sequence 2, Appli
19	567.5	77.0	152	4	US-10-642-124-2	Sequence 2, Appli
20	567.5	77.0	152	4	US-10-621-269-2	Sequence 2, Appli
21	567.5	77.0	152	4	US-10-620-850-2	Sequence 2, Appli
22	567.5	77.0	152	4	US-10-642-118-2	Sequence 2, Appli
23	567.5	77.0	152	4	US-10-642-119-2	Sequence 2, Appli
24	567.5	77.0	152	4	US-10-642-117-2	Sequence 2, Appli
25	567.5	77.0	152	5	US-10-642-099-2	Sequence 2, Appli
26	567.5	77.0	152	5	US-10-642-064-2	Sequence 2, Appli
27	567.5	77.0	152	5	US-10-642-116-2	Sequence 2, Appli
28	567.5	77.0	152	5	US-10-642-100-2	Sequence 2, Appli
29	567.5	77.0	152	5	US-10-642-058-2	Sequence 2, Appli
30	567.5	77.0	152	5	US-10-642-121-2	Sequence 2, Appli
31	567.5	77.0	152	5	US-10-642-065-2	Sequence 2, Appli
32	567.5	77.0	152	4	US-10-642-071-2	Sequence 2, Appl
33	564	76.5	138	4	US-10-389-155-72	Sequence 72, Appl
34	564	76.5	138	4	US-10-389-417-72	Sequence 72, Appl
35	562.5	76.3	133	5	US-10-452-357-85	Sequence 85, Appl
36	562.5	76.3	133	4	US-10-810-881A-79	Sequence 79, Appli
37	562	76.3	438	5	US-09-903-327A-6	Sequence 6, Appli
38	562	76.3	456	3	US-09-903-327A-13	Sequence 13, Appl
39	562	76.3	493	3	US-09-903-327A-12	Sequence 12, Appl
40	562	76.3	510	3	US-09-903-327A-11	Sequence 11, Appl
41	562	76.3	597	3	US-10-768-193	Sequence 14, Appl
42	562	76.3	613	3	US-09-903-327A-14	Sequence 14, Appl
43	557	75.6	132	5	US-09-982-107-14	Sequence 14, Appl
44	557	75.6	132	5	US-10-781-989-14	Sequence 14, Appl
45	554.5	75.2	137	4	US-10-462-062-158	Sequence 158, App

ALIGNMENTS

RESULT 1
US-10-768-193-7;

Sequence 7, Application US/10768193

; Publication No. US20040181042A1
; GENERAL INFORMATION:
; APPLICANT: MEDICAL & BIOLOGICAL LABORATORIES CO., LTD.
; APPLICANT: The director of Chubu National Hospital
; APPLICANT: YANAGISAWA, Katsuhiko
; APPLICANT: SHIBATA, Masao
; TITLE OF INVENTION: Antibody recognizing GM1 ganglioside-bound
; TITLE OF INVENTION: amyloid b-protein and DNA encoding the antibody
; FILE REFERENCE: P0102402
; CURRENT APPLICATION NUMBER: US/10/768,193
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: JP P2001-235700
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: PCT/JP02/07874
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 7
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-768-193-7 .

Query Match   100.0%; Score 737; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 2e-58;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYTMHWVKQSH 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYTMHWVKQSH 60

Qy   61 GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGAN 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGAN 120

Qy   121 WVFDYWGQGTTLTVSS 136
            ||||||||||||||||
Db   121 WVFDYWGQGTTLTVSS 136

RESULT 2
US-10-687-035-30

Sequence 30, Application US/10687035
; Publication No. US2005006451B A1
; GENERAL INFORMATION:
; APPLICANT: Albone, Earl F.
; APPLICANT: Soltis, Daniel A.

; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF
; FILE REFERENCE: 6750-214-999
; CURRENT APPLICATION NUMBER: US/10/687,035
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,986
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 60/418,828
; PRIOR FILING DATE: 2003-10-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSEQ for Windows Version 4.0
US-10-687-035-30
; SEQ ID NO 30
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 368.1 heavy chain polypeptide variable region (368.1H)

Query Match   86.9%;   Score 640.5;   DB 5;   Length 137;
Best Local Similarity   87.6%;   Pred. No. 9.1e-50;
Matches 120;   Conservative   8;   Mismatches   8;   Indels   1;   Gaps   1;

Qy   1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH 60
           |||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db   1 MGWIWIFLFLLSGTAGVHSEVQLVRTGASVKISCKASGYSFTGYYMHWVKQSL 60

Qy   61 GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCAR-GA 119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db   61 GKSLEWIGVSCYTGATTYTQKFKGKATFTVDTSSSTAYMQLNSLTSEDSAVYYCAREGD 120

Qy   120 NWVFDYWGQGTTLTVSS 136
           ||||||||||||:|||
Db   121 YYSMDFWGQGTSVTVSS 137

RESULT 3
US-10-462-062-153
; Sequence 153, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 153
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
; OTHER INFORMATION: sequence for H chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-2
US-10-462-062-153

Query Match   81.6%;   Score 601.5;   DB 4;   Length 137;
Best Local Similarity   83.2%;   Pred. No. 2.9e-46;
Matches 114;   Conservative   5;   Mismatches   17;   Indels   1;   Gaps   1;

Qy   1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH 60
           |||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db   1 MEWSWIFLFLLSGTTGVHSEIQLQQSGPELVKPGASVVSCKASGYSFTDYNMYWVKQSH 60

Qy   61 GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGA- 119

Db   61 GKSLEWIGYIDPYNGGTIYNQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGE 120

Qy   120 NWVFDYWGQGTTLTVSS 136
           :|||||||||||||||
Db   121 GYYFDYWGQGTSVTVSS 137

RESULT 4
US-10-462-062-154
; Sequence 154, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 154
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
; OTHER INFORMATION: sequence for H chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-3
US-10-462-062-154

Query Match   81.6%;   Score 601.5;   DB 4;   Length 137;
Best Local Similarity   83.2%;   Pred. No. 2.9e-46;
Matches 114;   Conservative   5;   Mismatches   17;   Indels   1;   Gaps   1;

Qy   1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH 60
           |||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db   1 MEWSWIFLFLLSGTTGVHSEIQLQQSGPELVKPGASVVSCKASGYSFTDYNMYWVKQSH 60

Qy   61 GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGA- 119
           ||||||||||| ||| |||||||||||||||:|:|||||:|||||||||||||||||||
Db   61 GKSLEWIGYIDPYNGGTIYNQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGE 120

Qy   120 NWVFDYWGQGTTLTVSS 136
           :|||||||||||||||
Db   121 GYYFDYWGQGTSVTVSS 137

RESULT 5
US-10-389-155-60
; Sequence 60, Application US/10389155
; Publication No. US20030229208A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Co, Man Sung
; Schneider, William P.
; Landolfi, Nicholas F.
; Coelingh, Kathleen L.
; Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: March 21, 2006, 18:05:40 ; Search time 35.4113 Seconds
    (without alignments)
    317.523 Million cell updates/sec

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Perfect Score: 737
Sequence: 1 MGWIWIFLFLLSGTAGVHSE..........RGANWVFDYWGQGTLLTVSS 136
Scoring table: BLOSUM62
    Gapop 10.0 , Gapext 0.5
Searched: 572060 seqs, 82675679 residues

Database :   Issued Patents AA:*
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Post-processing: Minimum Match 0%
    Maximum Match 100%
    Listing first 45 summaries

Minimum Match 0%
Maximum Match 100%

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters: 572060

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	593.5	81.5	137	2	US-09-647-468-154	Sequence 154, Appl
3	593.5	80.5	135	1	US-07-634-278-69	Sequence 69, Appl
4	593.5	80.5	135	1	US-08-477-728-69	Sequence 69, Appl
5	593.5	80.5	135	1	US-08-474-040-69	Sequence 69, Appl
6	593.5	80.5	135	1	US-08-487-200-69	Sequence 69, Appl
7	593.5	80.5	135	1	US-08-137-117D-27	Sequence 27, Appl
8	593.5	80.5	135	1	US-08-436-717-27	Sequence 27, Appl
9	593.5	80.5	135	2	US-08-484-537-69	Sequence 69, Appl
10	564	76.5	138	1	US-07-634-278-85	Sequence 85, Appl
11	564	76.5	138	1	US-08-477-728-85	Sequence 85, Appl
12	564	76.5	138	1	US-08-474-040-85	Sequence 85, Appl
13	564	76.5	138	1	US-08-487-200-85	Sequence 85, Appl
14	564	76.5	138	2	US-08-484-537-85	Sequence 85, Appl
15	557	75.6	132	2	US-08-434-000A-14	Sequence 14, Appl
16	557	75.6	132	2	US-09-312-157-14	Sequence 14, Appl
17	557	75.6	132	1	US-08-717-888-14	Sequence 14, Appl
18	555.5	75.4	137	2	US-08-379-057-18	Sequence 18, Appl
19	555.5	75.2	137	2	US-09-647-468-158	Sequence 158, App
20	554	75.2	142	2	US-08-678-194-8	Sequence 8, Appl
21	554	75.2	142	2	US-08-890-011-8	Sequence 8, Appl
22	554	75.2	142	2	US-09-262-724-8	Sequence 8, Appli
23	551.5	74.8	139	1	US-08-116-778E-1	Sequence 1, Appli
24	551.5	74.8	139	1	US-08-438-562-1	Sequence 1, Appli
25	551.5	74.7	139	1	US-08-483-528B-91	Sequence 91, Appli
26	550.5	74.7	137	1	US-08-116-778E-3	Sequence 3, Appli
27	550.5	74.7	137	1	US-08-438-562-3	Sequence 3, Appli
28	550.5	74.7	137	1	US-08-483-528B-93	Sequence 93, Appl
29	549.5	74.6	124	2	US-09-257-069-2	Sequence 2, Appli
30	549.5	74.6	124	2	US-10-007-790-2	Sequence 2, Appli
31	545.5	74.0	137	2	US-09-647-468-157	Sequence 157, App
32	544	73.8	136	4	PCT-US93-11612-4	Sequence 4, Appli
33	544	73.8	140	4	US-08-525-539A-47	Sequence 47, Appl
34	542	73.5	140	2	US-08-579-378A-4	Sequence 4, Appli
35	541.5	73.5	233	2	US-08-444-644-33	Sequence 33, Appl
36	541.5	73.5	233	2	US-08-232-246A-33	Sequence 33, Appl
37	541.5	73.5	235	2	US-08-444-644-19	Sequence 19, Appl
38	541.5	73.5	235	2	US-08-232-246A-19	Sequence 19, Appl
39	541.5	73.5	235	2	US-08-444-644-28	Sequence 28, Appl
40	541.5	73.5	235	2	US-08-232-246A-28	Sequence 28, Appl
41	541.5	73.5	235	2	US-08-444-644-42	Sequence 42, Appl
42	541.5	73.5	235	2	US-08-232-246A-42	Sequence 42, Appl
43	534.5	72.5	137	2	US-08-444-644-17	Sequence 17, Appl
44	534.5	72.5	137	2	US-08-232-246A-17	Sequence 17, Appl
45	526	71.4	140	2	US-08-836-561-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-647-468-153
Sequence 153, Application US/09647468 .....*
Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 0534667/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 153
LENGTH: 137
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence coding for H chain V region of ant-TF
OTHER INFORMATION: mouse monoclonal antibody ATR-2
US-09-647-468-153

Query Match   81.6%;   Score 601.5;   DB 2;   Length 137;
Best Local Similarity   83.2%;   Pred. No. 5.5e-48;
Matches 114;   Conservative   5;   Mismatches 17;   Indels   1;   Gaps   1;

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Qy    1  MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH  60
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Db    1  MEWSWIFLFLLSGTAGVHSEIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSH  60

Qy   61  GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGA   119
         |||||||||:  |||| :|||||||||| ||||  |||| |  |||||||||||||||||
Db   61  GKSLEWIGYIDPYNGGTIYNQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGE  120

Qy  120  NWVFDYWGQGTLLTVSS  136
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Db  121  GYYFDYWGQGTTLTVSS  137
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RESULT 2
US-09-647-468-154
Sequence 154, Application US/09647468
Patent No. 6677436

GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: 1999-04-03
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 154
LENGTH: 137
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence coding for H chain V region of ant-TF
OTHER INFORMATION: mouse monoclonal antibody ATR-3
US-09-647-468-154

Query Match   81.6%; Score 601.5; DB 2; Length 137;
Best Local Similarity   83.2%; Pred. No. 5.5e-48;
Matches 114; Conservative   5; Mismatches   17; Indels   1; Gaps   1;

Qy   1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH 60
         ||||||||||||| ||||||:|||||||||||:|||||::||||||||||:|| | |||||
Db   1 MEWSWIFLFLLSGVTGVHSEIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSH 60

Qy   61 GKSLEWIGYISCYNGATSYNQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCARGA- 119
         |||||||||:||||||||||||||||||||||:||||||:|||||||||||||||||||
Db   61 GKSLEWIGYIDPYNGGTIYNQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGE 120

Qy 120 NWVFDYWGQGTTLTVSS 136
          :|||||||||||||||
Db 121 GYYFDYWGQGTTLTVSS 137

RESULT 3
US-07-634-278-69
Sequence 69, Application US/0763278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-0002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-634-278-69

Query Match   80.5%; Score 593.5; DB 1; Length 135;
Best Local Similarity   83.8%; Pred. No. 2.9e-47;
Matches 114; Conservative   3; Mismatches   18; Indels   1; Gaps   1;

Qy   1 MGWIWIFLFLLSGTAGVHSEVQLQQSGPELVKTGASVKISCKASGYSFTGYYMHWVKQSH 60
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Qy 121 NWVFDYWGQGTTLTVSS 136
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RESULT 4
US-08-477-728-69
Sequence 69, Application US/0847728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: March 21, 2006, 17:50:10 ; Search time 286.234 Seconds
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Perfect score: 668
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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	601	90.0	131	6	AAW85058	Aaw85058 Mouse Br-
5	601	90.0	131	2	ABU58892	Abu58892 Mouse ant
6	599	89.7	128	2	AAR95949	Aar95949 3G3 varia
7	567	84.9	240	1	AAP80157	Aap80157 Biosynthe
8	557	83.4	261	3	AAY44990	Aay44990 Murine an
9	552	82.6	115	2	AAR05510	Aar05510 IGA type
10	545	81.6	269	2	AAR54756	Aar54756 pRAS111 b
11	545	81.6	415	2	AAR56484	Aar56484 ScFv pRAS
12	542	81.1	269	2	AAR56482	Aar56482 ScFv pRAS
13	535	80.1	112	8	AAR88720	Aar88720 Mouse ant
14	535	80.1	114	7	ADU39947	Adu39947 Antibody
15	535	80.1	243	8	ADM07541	Adm07541 Murine im
16	534	79.9	435	2	AAR56483	Aar56483 ScFv pRAS
17	532	79.6	256	2	ADT07627	Adt07627 Polypepti
18	532	79.6	256	2	AAR22568	Aar22568 ScFvB18 c
19	532	79.6	256	2	AAR22582	Aar22582 ScFvB18 c
20	532	79.6	428	2	AAW24027	Aaw24027 Single ch
21	532	79.6	443	2	AAW24025	Aaw24025 Single ch
22	531	79.5	110	2	ADU39960	Adu39960 Antibody
23	531	79.5	402	2	AAR56485	Aar56485 ScFv pRAS
24	530	79.3	239	8	ADT07625	Adt07625 Polypepti
25	530	79.3	239	9	ADW13546	Adw13546 Anti-anti
26	528	79.0	256	2	AAR22584	Aar22584 ScFvB18 c
27	527	78.9	230	7	ADM07543	Adm07543 Murine im
28	526	78.7	112	2	AAY03868	Aay03868 SM3 light
29	526	78.7	256	2	AAR22587	Aar22587 ScFvB18 c
30	526	78.7	256	2	AAR22585	Aar22585 ScFvB18 c
31	525	78.6	110	2	ADT07573	Adt07573 Polypepti
32	525	78.6	244	8	ADT07628	Adt07628 Polypepti
33	525	78.6	256	2	AAR22586	Aar22586 ScFvB18 c
34	523	78.3	229	7	ADM07542	Adm07542 Murine im
35	523	78.3	229	7	ADM07544	Adm07544 Murine im
36	522	78.1	109	9	ADW13535	Adw13535 Anti-anti
37	522	78.1	110	2	AAR05038	Aar05038 Metal che
38	522	78.1	256	2	AAR54136	Aar54136 CHA255 li
39	522	78.1	256	2	AAR22583	Aar22583 ScFvB18 c
40	521	78.0	272	7	ADE29203	Ade29203 Multivale
41	521	78.0	273	4	AAB70763	Aab70763 Single ch
42	520	77.8	110	2	AAR04938	Aar04938 Chelate-s
43	520	77.8	110	8	ADT07571	Adt07571 Polypepti
44	520	77.8	240	8	ADT07626	Adt07626 Polypepti
45	519	77.7	110	8	ADR73591	Adr73591 Anti-AR a

ALIGNMENTS

RESULT 1
ABU08928
ID   ABU08928 standard; protein; 129 AA.
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AC   ABU08928;
XX
DT   03-JUN-2003 (first entry)
XX
DE   Mouse amyloid beta antibody light chain variable region.
XX
KW   Mouse; antibody; beta-amyloid fibril inhibitor; Alzheimer's disease;
KW   GM1 ganglioside-bound amyloid beta protein; amyloid beta protein;
KW   amyloid fibril formation inhibition; light chain; variable region.
XX
OS   Mus musculus.
XX
FH   Key   Location/Qualifiers
FH
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FT   /label= Signal_sequence
FT   Protein   20..129
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FT   antibody light chain variable region."
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FT   /label= CDR1
FT   /note= "Complementarity determining region 1.
FT   Specifically claimed in claim 2"
FT   Region   71..77
FT   /label= CDR2
FT   /note= "Complementarity determining region 2.
FT   Specifically claimed in claim 2"
FT   Region   110..118
FT   /label= CDR3
FT   /note= "Complementarity determining region 3.
FT   Specifically claimed in claim 2"
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PN   WO2003014162-A1.
XX
PD   20-FEB-2003.
XX
PF   01-AUG-2002; 2002WO-JP007874.
XX
PR   03-AUG-2001; 2001JP-00235700.
XX
PA   (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
PA   (NICH-) JAPAN CHUBU NAT HOSPITAL.
PA   (YANA/) YANAGISAWA K.
XX

PI   Yanagisawa K, Shibata M;
XX
DR   WPI; 2003-268182/26.
DR   N-PSDB; ABX93689.
XX
PT   Antibodies recognizing GM1 ganglioside-bound amyloid beta-protein and
PT   encoded DNAs, useful in diagnosing, preventing or treating Alzheimer's
PT   disease by inhibiting early-stage beta-amyloid fibril formation.
XX
PS   Claim 5; Fig 2; 60pp; Japanese.
XX
CC   The invention relates to four antibodies recognising GM1 ganglioside-
CC   bound amyloid beta protein and having inhibitory activity on the
CC   formation of amyloid fibril. The antibodies are useful in diagnosing,
CC   preventing or treating Alzheimer's disease by inhibiting early-stage beta
CC   -amyloid fibril formation. The antibody does not recognise soluble
CC   amyloid beta-protein, and thus drugs produced from the antibodies are
CC   efficacious in treating Alzheimer's disease. The present sequence
CC   represents the amino acid sequence of mouse GM1 ganglioside-bound amyloid
CC   beta antibody light chain variable region
XX
SQ   Sequence 129 AA;

Query Match   100.0%; Score 668; DB 6; Length 129;
Best Local Similarity   100.0%; Pred. No. 3.4e-51;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFG 120
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Db   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFG 120

Qy 121 GGTKVTVLG 129
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Db 121 GGTKVTVLG 129

RESULT 2
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ID   AAR09422 standard; protein; 131 AA.
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AC   AAR09422;
XX
DT   25-MAR-2003 (revised)
DT   04-MAR-1993 (first entry)
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DE   Br-3 Light Chain V Region (mouse).
XX
KW   Monoclonal antibody; chimera; light; heavy; chain; constant; variable;
KW   antigen; diagnosis; cancer; tumour.
XX
OS   Mus musculus.
XX
PN   WO9002569-A.
XX
PD   22-MAR-1990.
XX
PF   08-SEP-1988.
XX
PR   08-SEP-1988;   88US-00241744.
PR   13-SEP-1988;   88US-00243739.
PR   04-OCT-1988;   88US-00253002.
PR   19-JUN-1989;   89US-00367641.
PR   21-JUL-1989;   89US-00382768.
XX
PA   (ITGE-) INT GENETIC ENG INC.
PA   (INGE-) INGENE INT GENETIC.
XX
PI   Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;

DR   WPI; 1990-115825/15.
DR   N-PSDB; AAQ08604.
XX
PT   Chimeric mouse-human antibodies - prepd. using genes coding for constant
PT   human region murine variable region, esp. to 3 tumour antigen.
XX
PS   Claim 13; Page 123 + Fig 14; 173pp; English.
XX
CC   The sequence is used in the prodn. of a chimeric antibody mol. comprising
CC   two light chains and two heavy chains, each having a constant region
CC   (human) and a variable region (murine) having specificity to an antigen
CC   bound by murine monoclonal antibody (MAb) Br-3. The chimeric antibodies
CC   can be used for any purpose for which the original murine MAbs can be
CC   used, with the advantage that they are more compatible with the human
CC   body. They are esp. used for the diagnosis and treatment of cancer.
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 131 AA;

Query Match   89.9%; Score 601; DB 2; Length 131;
Best Local Similarity   89.9%; Pred. No. 2.9e-45;
Matches 116; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy   1 MAWTSLILSLLALCSGASSQAVVTQESALTTSPGGTVILTCRSSSTGAVTTSNYANWVQEK 60
         ||||||||||||||||| :|||||||||:||||||||||||||||||||||||||||||||
Db   1 MAWTSLILSLLALCSGAISQAVVTQESALTTSPGETVTLTCRSSSTGAVTTSNYANWVQEK 60

Qy   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFG 120
         ||||||||||||:|||||||:|||||||||||||||| :|||:||:||||||||: ||||
Db   61 PDHLFTGLIGGTNNRAPGVPARFSGSLIGDKAALTITGTQTEDEAIYFCALWYSNHWFG 120

Qy 121 GGTKVTVLG 129
         ||||:|||||
Db 121 GGTKLITVLG 129

RESULT 3
AAW06211
ID   AAW06211 standard; protein; 131 AA.
XX
AC   AAW06211;
XX
DT   25-MAR-2003 (revised)
DT   12-FEB-1997 (first entry)
XX
DE   MAb Br-3 light chain variable region.
XX
KW   Chimeric antibody; monoclonal antibody; Br-3; antibody engineering;
KW   tumour; antigen; breast carcinoma; lung carcinoma; colon carcinoma;
KW   ovary carcinoma; cancer; diagnosis; therapy; light chain.
XX
OS   Mus sp.
XX
PN   US5576184-A.
XX
PD   19-NOV-1996.
XX
PF   27-DEC-1994;   94US-00364001.
XX
PR   06-SEP-1988;   88US-00240624.
PR   08-SEP-1988;   88US-00241744.
PR   13-SEP-1988;   88US-00243739.
PR   04-OCT-1988;   88US-00253002.
PR   19-JUN-1989;   89US-00367641.
PR   21-JUL-1989;   89US-00382768.
PR   06-MAY-1991;   91US-00659401.
XX
PA   (XOMA) XOMA CORP.
XX
PI   Chang CP, Lei S, Better MD, Robinson RR, Horwitz AH;
XX
DR   WPI; 1997-011249/01.
DR   N-PSDB; AAT43436.

OM protein - protein search, using sw model

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GenCore version 5.1.7

Run on: March 21, 2006, 18:00:46 ; Search time 23.8528 Seconds
                                         (without alignments)
                                         520.356 Million cell updates/sec

Title: US-10-768-193-8
Perfect score: 668
Sequence: 1 MAWTSLILSLLALCSGASSQ.........ALWYSTHYVFGGGTKVTVLG 129

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
               1: pir1:*
               2: pir2:*
               3: pir3:*
               4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	649	97.2	129	1	L2MS35	Ig lambda-2 chain
2	603	90.3	117	1	L2MSWE	Ig lambda-2 chain
3	599	89.7	128	2	S52450	Ig lambda chain V
4	597	89.4	129	1	L1MS4E	Ig lambda-1 chain
5	545	81.6	116	1	L1MSV	Ig lambda-1 chain
6	529	79.2	287	4	PC4402	pelB leader/Ig hea
7	525	78.6	100	2	PH1087	Ig lambda chain
8	518	77.5	113	2	S05819	Ig lambda chain V
9	514	76.9	214	2	PC4156	Ig lambda chain V
10	511.5	76.6	112	2	S06818	Ig lambda chain V
11	506.5	75.8	114	2	S06820	Ig lambda chain V
12	506	75.7	106	2	S20654	Ig lambda chain V
13	503	75.3	99	2	S14583	Ig lambda chain V
14	497.5	74.5	114	2	S06822	Ig lambda chain V
15	492	73.7	113	2	B54256	Ig lambda-1 chain
16	492	73.7	113	2	S06821	Ig lambda chain V
17	485	72.6	92	2	A27633	Ig lambda-2 chain
18	482	72.2	116	2	C27390	Ig lambda chain
19	477	71.4	99	2	S14582	Ig lambda chain pr
20	475	71.1	97	2	PH1090	Ig lambda chain
21	475	71.1	100	2	PH1088	Ig lambda chain
22	470	70.4	99	2	S14584	Ig lambda chain V
23	470	70.4	99	2	PH1089	Ig lambda chain V
24	469.5	70.3	99	2	S14586	Ig lambda chain V
25	454	68.0	99	2	S14585	Ig lambda chain V
26	444	66.5	136	2	S42610	ARMV1lambda protein
27	351.5	52.6	117	1	S04526	Ig lambda chain pr
28	348	52.1	117	1	LVHU2	Ig lambda chain pr
29	336.5	50.4	235	2	S25749	Ig lambda chain -
30	302.5	45.3	120	2	S30528	Ig lambda chain v
31	289.5	43.3	127	2	S70444	Ig lambda chain pr
32	289	43.3	98	2	S36062	Ig lambda chain -
33	289	43.3	112	2	S26655	Ig lambda chain V
34	287.5	43.0	110	2	S74465	Ig lambda chain v-
35	283.5	42.4	233	2	S25741	Ig lambda chain -
36	282.5	42.3	231	2	S25738	Ig lambda chain -
37	273.5	40.9	151	2	S25751	Ig lambda chain -
38	267.5	40.0	231	2	S25739	Ig lambda chain -
39	266.5	39.9	233	2	S25747	Ig lambda chain -
40	265.5	39.7	233	2	S25748	Ig lambda chain -
41	264.5	39.6	128	2	S24319	Ig lambda chain pr
42	264	39.5	98	2	S36063	Ig lambda chain -
43	262	39.2	235	2	S25754	Ig lambda chain -
44	260.5	39.0	132	2	S09713	Ig lambda chain V
45	260.5	39.0	233	2	S25744	Ig lambda chain -

ALIGNMENTS

RESULT 1
L2MS35

Ig lambda-2 chain precursor V region (MOPC 315) - mouse
C;Species: Mus musculus (house mouse)
A;Note: the sequence was determined from the differentiated gene
R;Schechter, I.; Wolf, O.; Zemell, R.; Burstein, Y.
Fed. Proc. 38, 1839-1845, 1979
A;Title: Structure and function of immunoglobulin genes and precursors.
R;Wu, G.E.; Govindji, N.; Hozumi, N.; Murialdo, H.
Nucleic Acids Res. 10, 3831-3843, 1982
A;Title: Nucleotide sequence of a chromosomal rearranged lambda-2 immunoglobulin gene of
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D
Nature 298, 380-382, 1982
A;Title: Somatic variants of murine immunoglobulin lambda light chains.
A;Reference number: A93282; MUID:82220143; PMID:6283385
A;Accession: B93282
A;Molecule type: DNA
A;Residues: 1-129 <BOT>
A;Cross-references: UNIPARC:UPI000017724
R;Dugan, E.S.; Bradshaw, R.A.; Simms, E.S.; Eisen, H.N.
Biochemistry 12, 5400-5416, 1973
A;Title: Amino acid sequence of the light chain of a mouse myeloma protein (MOPC-315).
A;Reference number: A90372; MUID:74048693; PMID:4760498
A;Accession: A90372
A;Molecule type: protein
A;Residues: 20-24, E',26-73,'D',75-129 <DUG>
A;Cross-references: UNIPARC:UPI000173725
R;Gavish, M.; Zakut, R.; Wilchek, M.; Givol, D.
Biochemistry 17, 1345-1351, 1978
A;Title: Preparation of a semisynthetic antibody.
A;Reference number: A90410; MUID:78187254; PMID:418802
A;Accession: A90410
A;Molecule type: protein
A;Residues: 1-129 <GAV>
A;Cross-references: UNIPARC:UPI0000270BD
R;Bogen, B.; Lambris, J.D.
EMBO J. 8, 1947-1952, 1989
A;Title: Minimum length of an idiotypic peptide and a model for its binding to a major h
A;Reference number: S09391; MUID:90005397; PMID:2792076
A;Accession: S09391

R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D
Nature 298, 380-382, 1982
A;Title: Somatic variants of murine immunoglobulin lambda light chains.
A;Reference number: A93282; MUID:82220143; PMID:6283385
A;Accession: B93282
A;Molecule type: DNA
A;Residues: 1-129 <BOT>
A;Cross-references: UNIPARC:UPI0000270BD
A;Reference number: A93431; MUID:82274221; PMID:6287422
A;Accession: A93431
A;Molecule type: mRNA
A;Residues: 1-129 <WUG>
R;Wu, G.E.; Govindji, N.; Hozumi, N.; Murialdo, H.
Nucleic Acids Res. 10, 3831-3843, 1982
A;Cross-references: B91462; MUID:79148758; PMID:428562
A;Accession: B91462
A;Reference number: A91462; MUID:79148758; PMID:428562
A;Title: Structure and function of immunoglobulin genes and precursors.
R;Schechter, I.; Wolf, O.; Zemell, R.; Burstein, Y.
Fed. Proc. 38, 1839-1845, 1979
A;Note: the sequence was determined from the differentiated gene
C;Species: Mus musculus (house mouse)
Ig lambda-2 chain precursor V region (MOPC 315) - mouse

A;Molecule type: protein
A;Residues: 110-126 <BOG>
A;Cross-references: UNIPARC:UPI000001073726
C;Comment: This chain is from a myeloma protein with anti-DNP activity.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin; immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; pyroglutamic acid
A;Superfamily: immunoglobulin; immunoglobulin V region; immunoglobulin homology
A;Description: heterotetramer; pyroglutamic acid
A;Reference number:
F;1-19/Domain: signal sequence #status experimental <SIG>
F;20-129/Domain: Ig lambda-2 chain precursor V region #status experimental <MAT>
F;34-111/Region: idiotype to histocompatibility complex class II #status experiment
F;20/Modified site: Pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F;41-109/Disulfide bonds: #status predicted

Query Match
Best Local Similarity   97.2%;
Matches 124;   Conservative 3;   Mismatches 2;   Indels 0;   Gaps 0;

```
Qy    1 MAWTSILILSLLALCSGASSQAVVTQESALTTSPGGTVILTCRSSSTGAVTTSNYANWVQEK 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||: |||
Db    1 MAWTSILILSLLALCSGASSQAVVTQESALTTSPGGTVILTCRSSSTGAVTTSNYANWIQEK 60

Qy   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHVFG 120
          |||||||||||||||||||||||||||||||||||||||||||||: :|||
Db   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWFRNHFVFG 120

Qy  121 GGTKVTVLG 129
          |||||||||
Db  121 GGTKVTVLG 129
```

RESULT 2
L2MSWE
Ig lambda-2 chain precursor V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
R;Tonegawa, S.; Maxam, A.M.; Tizard, R.; Bernard, O.; Gilbert, W.
R;Title: Sequence of a mouse germ-line gene for a variable region of an immunoglobulin 1
A;Reference number: A01996; MUID:78179064; PMID:418414
A;Accession: A01996
A;Molecule type: DNA
A;Residues: 1-117 <TON>
A;Cross-references: UNIPROT:P01728; UNIPARC:UPI000002IFB0; GB:V00815; NID:g52278; PIDN:C
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Introns: 16/1

S52450
Ig lambda chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52450
R;Berdoz, J.; Kraehenbuhl, J.P.
C;Accession: S52450
C;Comment: Specific amplification by the polymerase chain reaction of rearranged gen
submitted to the EMBL Data Library, November 1994
A;Reference number: S52450
A;Accession: S52445
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-128 <BBR>
A;Cross-references: UNIPARC:UPI000001148F; EMBL:X82687; NID:g673448; PIDN:CAA58008.1; PII

Query Match
Best Local Similarity   96.1%;   Score 649;   DB 1;   Length 129;
Matches 124;   Conservative 3;   Pred. No. 1.2e-48;   Mismatches 2;   Indels 0;   Gaps 0;

```
Qy    1 MAWTSILILSLLALCSGASSQAVVTQESALTTSPGGTVILTCRSSSTGAVTTSNYANWVQEK 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||: |||
Db    1 MAWTSILILSLLALCSGASSQAVVTQESALTTSPGGTVILTCRSSSTGAVTTSNYANWIQEK 60

Qy   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHVFG 120
          |||||||||||||||||||||||||||||||||||||||||||||: :|||
Db   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWFRNHFVFG 120

Qy  121 GGTKVTVLG 129
          |||||||||
Db  121 GGTKVTVLG 129
```

Query Match
Best Local Similarity   90.3%;   Score 603;   DB 1;   Length 117;
Matches 116;   Conservative 1;   Pred. No. 9e-45;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy    1 MAWTSILILSLLALCSGASSQAVVTQESALTTSPGGTVILTCRSSSTGAVTTSNYANWVQEK 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    1 MAWTSILILSLLALCSGASSQAVVTQESALTTSPGGTVILTCRSSSTGAVTTSNYANWVQEK 60

Qy   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHY 117
          |||||||||||||||||||||||||||||||||||||||||||||||: 
Db   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHF 117
```

RESULT 3

RESULT 4
L1MS4B
Ig lambda-1 chain precursor V regions (MOPC 104E, RPC20, J558, S104, S178, H2020, S43) -
C;Species: Mus musculus (house mouse)
C;Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004
C;Accession: B93815; B93775; C93775; A93784; B93784; A90780; C93282; A01995
R;Burstein, Y.; Schechter, I.
R;Title: Amino acid sequence of the NH2-terminal extra piece segments of the precursors
A;Reference number: A93815; MUID:77148916; PMID:403522
A;Contents: MOPC 104E
A;Accession: B93815
A;Molecule type: protein
A;Residues: 1-29 <BUR>
A;Cross-references: UNIPROT:P01724; UNIPARC:UPI000001173721
A;Note: this precursor was synthesized in a cell-free system directed by messenger RNA i
d after synthesis
R;Appella, E.
R;Title: Amino acid sequences of two mouse immunoglobulin lambda chains.
R;Reference number: A93775; MUID:71107854; PMID:5276767
A;Contents: MOPC 104E; RPC 20
A;Accession: B93775
A;Molecule type: protein
A;Residues: 21-25,'Q',27-129 <APP>
A;Cross-references: UNIPARC:UPI000001173722
A;Accession: C93775

Query Match
Best Local Similarity   90.8%;   Score 599;   DB 2;   Length 128;
Matches 116;   Conservative 5;   Pred. No. 2.2e-44;   Mismatches 7;   Indels 0;   Gaps 0;

```
Qy    1 MAWTSILILSLLALCSGASSQAVVTQESALTTSPGGTVILTCRSSSTGAVTTSNYANWVQEK 60
          |||||||||||||||||||||||||||||||||: ::|||||: :|||||||||||||||
Db    1 MAWISLILSLLALCSGAISOAVVTQESALTTSPGEEVTLTCRSSSTGAVTTSNYANWVQEK 60

Qy   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHVFG 120
          |||||||||||||||: :||||||||||||||||||||||||||||: :|||
Db   61 PDHLFTGLIGGTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFG 120
```

A;Molecule type: protein
A;Residues: 20-129 <AP2>
A;Cross-references: UNIPARC:UPI000001173722
A;Note: compositions and partial sequences of RPC 20 show no differences from MOPC 104E
R;Cesari, I.M.; Weigert, M.
R;Title: Mouse lambda-chain sequences.
R;Reference number: A93784; MUID:73229669; PMID:4516208
A;Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973
A;Contents: J558; S104; S178

```
Qy  121 GGTKVTVLG 129
          ||| |||
Db  121 GGTKLTVL 128
```

Query Match
Best Local Similarity   89.7%;
Matches 116;   Conservative 5;   Mismatches 7;   Indels 0;   Gaps 0;

```
Qy  121 GGTKVTVL 128
          ||| |||
Db  121 GGTKLTVL 128
```

RESULT 3 (Qy/Db lower-left)
```
Qy   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHY 117
Db   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHF 117
```

OM protein - protein search, using sw model

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GenCore version 5.1.7

Run on: March 21, 2006, 17:50:40 ; Search time 143.604 Seconds
(without alignments)
633.780 Million cell updates/sec

Title:
Perfect score: 668
Sequence: 1 MAWTSLILSLLALCSGASSQ..........ALWYSTHYVFGGGTKVTVLG 129

Title: US-10-768-193-8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt.05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	649	97.2	129	1	LV2B_MOUSE	P01729 mus musculu
2	605	90.6	129	1	LV1E_MOUSE	P01727 mus musculu
3	603	90.3	129	1	LV2A_MOUSE	P01728 mus musculu
4	598	89.5	117	1	LV1D_MOUSE	P01726 mus musculu
5	597	89.5	129	1	LV1B_MOUSE	P01724 mus musculu
6	593	88.8	129	1	Q8VDE2_MOUSE	Q8VDE2 mus musculu
7	534.5	80.0	117	1	LV1A_MOUSE	P01723 mus musculu
8	510	76.3	110	1	LV1C_MOUSE	P01725 mus musculu
9	509.5	76.3	113	2	Q8CGS1_MOUSE	Q8CGS1 mus musculu
10	495.5	74.2	109	2	Q9ET13_MOUSE	Q9ET13 mus musculu
11	366	54.8	234	2	Q5C294_HUMAN	Q5C294 homo sapien
12	339.5	50.8	117	1	LV0A_HUMAN	P04211 homo sapien
13	291	43.6	98	1	Q5NV80_HUMAN	Q5NV80 homo sapien
14	287	43.0	98	1	Q5NV83_HUMAN	Q5NV83 homo sapien
15	276	41.4	233	2	Q6GMW4_HUMAN	Q6GMW4 homo sapien
16	276	41.3	233	2	Q6GMX4_HUMAN	Q6GMX4 homo sapien
17	273.5	40.9	231	2	Q6GNB8_XENLA	Q6GNB8 xenopus lae
18	270.5	40.5	248	2	Q7SYU1_XENLA	Q7SYU1 xenopus lae
19	270	40.4	236	2	Q6GMV7_HUMAN	Q6GMV7 homo sapien
20	268.5	40.2	233	2	Q8TBC9_HUMAN	Q8TBC9 homo sapien
21	268.5	40.2	245	2	Q6GNC5_XENLA	Q6GNC5 xenopus lae
22	268	40.1	233	2	Q6PJA3_HUMAN	Q6PJA3 homo sapien
23	265.5	39.7	235	2	Q6PIK1_HUMAN	Q6PIK1 homo sapien
24	265	39.7	236	2	Q96E61_HUMAN	Q96E61 homo sapien
25	265	39.7	236	2	Q6PIQ7_HUMAN	Q6PIQ7 homo sapien
26	264.5	39.6	233	2	Q8N5F4_HUMAN	Q8N5F4 homo sapien
27	264	39.5	99	2	Q5NV62_HUMAN	Q5NV62 homo sapien
28	264	39.5	236	2	Q61PQ0_HUMAN	Q61PQ0 homo sapien
29	262	39.2	236	2	Q6PS83_HUMAN	Q6PS83 homo sapien
30	262	39.2	236	2	Q8NEJ1_HUMAN	Q8NEJ1 homo sapien
31	260	38.9	236	2	Q6GMX3_HUMAN	Q6GMX3 homo sapien
32	259	38.8	131	1	LV6E_HUMAN	P06319 homo sapien
33	259	38.8	232	2	Q5FWF9_HUMAN	Q5FWF9 homo sapien
34	255	38.2	234	2	Q8N355_HUMAN	Q8N355 homo sapien
35	254.5	38.1	235	2	Q567P1_HUMAN	Q567P1 homo sapien
36	253.5	37.9	233	2	Q6GNH3_XENLA	Q6GNH3 xenopus lae
37	252.5	37.8	130	1	LV1G_HUMAN	P06316 homo sapien
38	252.5	37.8	235	2	Q6GMW6_HUMAN	Q6GMW6 homo sapien
39	251	37.6	235	2	Q6GMW3_HUMAN	Q6GMW3 homo sapien
40	249.5	37.4	235	2	Q6IN99_HUMAN	Q6IN99 homo sapien
41	248	37.1	234	2	Q6GMV8_HUMAN	Q6GMV8 homo sapien
42	246.5	36.9	233	2	Q6NS96_HUMAN	Q6NS96 homo sapien
43	246.5	36.9	235	2	Q6PJG0_HUMAN	Q6PJG0 homo sapien
44	240.5	36.0	111	1	LV6C_HUMAN	P06317 homo sapien
45	240.5	36.0	148	2	Q6PJ28_HUMAN	Q6PJ28 homo sapien

ALIGNMENTS

RESULT 1
LV2B_MOUSE

ID   LV2B_MOUSE   STANDARD;   PRT;   129 AA.
AC   P01729;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig lambda-2 chain V region MOPC 315 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=82220143; PubMed=6283385;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Somatic variants of murine immunoglobulin lambda light chains.";
RL   Nature 298:380-382(1982).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 1-22.
RX   MEDLINE=79148758; PubMed=428562;
RA   Schechter I., Wolf O., Zemell R., Burstein Y.;
RT   "Structure and function of immunoglobulin genes and precursors.";
RL   Fed. Proc. 38:1839-1845(1979).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 20-129.
RX   MEDLINE=74048693; PubMed=4760498;
RA   Dugan E.S., Bradshaw R.A., Simms E.S., Eisen H.N.;
RT   "Amino acid sequence of the light chain of a mouse myeloma protein
RT   (MOPC-315).";
RL   Biochemistry 12:5400-5416(1973).
RN   [4]
RP   PROTEIN SEQUENCE OF 20-129.
RX   MEDLINE=78187254; PubMed=418802;
RA   Gavish M., Zakut R., Wilchek M., Givol D.;
RT   "Preparation of a semisynthetic antibody.";
RL   Biochemistry 17:1345-1351(1978).
RN   [5]
RP   DETERMINATION OF AMIDATION STATES OF 58; 59; 62; 100; 102 AND 115.
RA   Wu G.E., Govindji N., Hozumi N., Murialdo H.;
RT   "Nucleotide sequence of a chromosomal rearranged lambda 2
RT   immunoglobulin gene of mouse.";
RL   Nucleic Acids Res. 10:3831-3843(1982).
CC   -!- MISCELLANEOUS: This chain is from a myeloma protein with anti-DNP
CC   activity.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not

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CC   removed.
DR   PIR; A93431; L2MS35.
DR   HSSP; P01724; 1A6V.
DR   SMR; P01729; 20-129.
DR   Ensembl; ENSMUSG00000064012; Mus musculus.
DR   InterPro; IPR002197; HTH_Fis.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig-v.
DR   PRINTS; PR01590; HTHFIS.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid; Signal.
KW   Direct protein sequencing; Immunoglobulin domain;
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FT   SIGNAL        1     19
FT   CHAIN        20    129       Ig lambda-2 chain V region MOPC 315.
FT   DOMAIN       20    125       Ig-like.
FT   MOD_RES      20     20       Pyrrolidone carboxylic acid.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  13418 MW;  0AA6B812S723552C CRC64;
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Query Match             97.2%;
Best Local Similarity   96.1%;
Matches  124;  Conservative   3;  Mismatches   2;  Indels   0;  Gaps   0;
Score 649;  DB 1;  Length 129;

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Db   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWFRNHFVFG 120

Qy  121 GGTKVTVLG 129
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Db  121 GGTKVTVLG 129
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RESULT 2
LV1E_MOUSE    STANDARD;    PRT;   129 AA.
AC   P01727;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig lambda-1 chain V region S43 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RL   Nature 298:380-382(1982).
RT   "Somatic variants of murine immunoglobulin lambda light chains.";
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RX   MEDLINE=82220143; PubMed=6283385;
RP   NUCLEOTIDE SEQUENCE.
RN   [1]
```

```
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    129       Ig lambda-1 chain V region S43.
FT   DOMAIN       20    125       Ig-like.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  13529 MW;  84E54E7DD5791345 CRC64;
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Best Local Similarity   90.7%;
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Score 605;  DB 1;  Length 129;

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Qy   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFG 120
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Db   61 PDHLFTGLIGGTNNRAPGVPARFSGSLIGDKAALTITGTQTEDEAMYFCALWYSNHVFG 120

Qy  121 GGTKVTVLG 129
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Db  121 GGTKVTVLG 129
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AC   P01728;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig lambda-2 chain V region precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=78179064; PubMed=418414;
RA   Tonegawa S., Maxam A.M., Tizard R., Bernard O., Gilbert W.;
RT   "Sequence of a mouse germ-line gene for a variable region of an
RT   immunoglobulin light chain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 75:1485-1489(1978).
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DR   EMBL; J00599; AAA39167.1; -; Genomic_DNA.
DR   EMBL; V00815; CAA24196.2; -; Genomic_DNA.
DR   EMBL; X58412; CAA41113.1; -; Genomic_DNA.
DR   EMBL; X58418; CAA41318.1; -; Genomic_DNA.
DR   EMBL; X58423; CAA41323.1; -; Genomic_DNA.
DR   EMBL; X58424; CAA41324.1; -; Genomic_DNA.
DR   PIR; A01996; L2MSWE.
DR   HSSP; P01724; 1A6V.
DR   SMR; P01728; 20-117.
DR   Ensembl; ENSMUSG00000064012; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig-v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       Ig lambda-2 chain V region.
FT   DOMAIN       20   >117       Ig-like.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12222 MW;  43FDF19741B942A6 CRC64;
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 21, 2006, 18:05:40 ; Search time 33.5887 Seconds
(without alignments)
317.523 Million cell updates/sec

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Perfect score: 668
Sequence: 1 MAWTSLILSLLALCSGASSQ.........ALWYSTHYFGGGTKVTVLG 129

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	597	89.4	128	2	US-08-348-548-2	Sequence 2, Appli
2	597	89.4	128	4	PCT-US95-15716-2	Sequence 3, Appli
3	552	82.6	115	2	5215889-3	Sequence 121, App
4	552	82.6	269	1	Patent No. 5215889	Patent No. 5215889
5	545	81.6	269	1	US-08-428-257A-72	Sequence 72, Appl
6	545	81.6	402	1	US-08-491-988-3	Sequence 3, Appli
7	545	81.6	415	1	US-08-491-988-9	Sequence 9, Appli
8	545	81.6	415	1	US-08-491-988-7	Sequence 7, Appli
9	545	81.6	435	1	US-08-491-988-5	Sequence 5, Appli
10	535	80.1	112	2	US-09-157-370-6	Sequence 6, Appli
11	512	76.6	109	2	US-09-232-290-14	Sequence 14, Appl
12	507	75.9	110	1	US-08-122-546-14	Sequence 14, Appl
13	507	75.9	110	1	US-08-764-938-14	Sequence 14, Appl
14	507	75.9	110	2	US-09-131-052-14	Sequence 14, Appl
15	507	75.9	111	2	US-09-131-053A-14	Sequence 14, Appl
16	503.5	75.4	110	2	US-09-232-290-11	Sequence 11, Appl
17	495.5	74.2	109	2	US-09-865-483-7	Sequence 7, Appl
18	495.5	74.2	109	2	US-10-726-555-7	Sequence 7, Appli
19	495	74.1	106	1	US-08-440-354-2	Sequence 2, Appli
20	495	74.1	106	1	US-08-463-087-2	Sequence 2, Appli
21	490	73.4	109	1	US-08-672-345C-1	Sequence 1, Appli
22	490	73.4	109	2	US-09-214-095D-1	Sequence 1, Appli
23	490	73.4	109	1	US-09-940-727B-1	Sequence 1, Appli
24	486	72.8	109	1	US-08-672-345C-2	Sequence 2, Appli
25	486	72.8	109	2	US-09-214-095D-2	Sequence 2, Appli
26	486	72.8	109	1	US-09-940-727B-2	Sequence 2, Appli
27	477	71.4	109	1	US-08-672-345C-3	Sequence 3, Appli
28	477	71.4	109	2	US-09-214-095D-3	Sequence 3, Appli
29	477	71.4	109	2	US-09-940-727B-3	Sequence 3, App
30	477	71.4	109	2	US-09-940-727B-121	Sequence 121, App
31	475	71.1	109	1	US-08-672-345C-93	Sequence 93, Appl
32	462	69.2	109	1	US-08-428-257A-72	Sequence 72, Appli
33	446	66.8	99	1	US-08-672-345C-4	Sequence 4, Appli
34	446	66.8	99	1	US-09-214-095D-4	Sequence 4, Appli
35	446	66.8	99	1	US-09-940-727B-4	Sequence 4, Appli
36	442	66.2	99	2	US-08-672-345C-94	Sequence 94, Appli
37	442	66.2	99	2	US-09-214-095D-88	Sequence 88, Appl
38	442	66.2	200	6	5189147-10	Patent No. 5189147
39	423.5	63.4	99	1	US-08-672-345C-92	Sequence 92, Appl
40	414	62.0	100	1	US-09-214-095D-96	Sequence 96, Appli
41	414	62.0	100	2	US-09-940-727B-96	Sequence 96, Appli
42	412	61.7	99	1	US-08-672-345C-94	Sequence 94, Appli
43	402	60.2	98	2	US-09-214-095D-4	Sequence 4, Appli
44	402	60.2	98	2	US-09-940-727B-4	Sequence 4, Appli
45	368.5	55.2	240	2	US-09-049-672A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-348-548-2
Sequence 2, Application US/08348548
Patent No. 6258529
GENERAL INFORMATION:
  APPLICANT: Berdoz, Jose
  APPLICANT: Kraehenbuhl, Jean Pierre
  TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
  TITLE OF INVENTION: VARIABLE REGIONS, OF IMMUNOGLOBULIN GENES
  NUMBER OF SEQUENCES: 108
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Fish & Richardson
  STREET: 225 Franklin Street, Suite 3100
  CITY: Boston
  STATE: MA
  COUNTRY: USA
  ZIP: 02110-2804
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
  CURRENT APPLICATION NUMBER: US/08/348,548
  APPLICATION NUMBER: US/08/348,548
  FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
  NAME: Clark, Paul T.
  REGISTRATION NUMBER: 30,162
  REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (617) 542-5070
  TELEFAX: (617) 542-5070
  TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 128 amino acids
  TYPE: amino acid
  STRANDEDNESS: not relevant
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-348-548-2

Query Match   89.4%;   Score 597;   DB 2;   Length 128;
Best Local Similarity   90.6%;   Pred. No. 4.4e-50;
Matches 116;   Conservative   4;   Mismatches   8;   Indels   0;   Gaps   0;

Qy   1 MAWTSLILSLLALCSGASSQAVVTQESALTTSPGGTVILTCRSSTGAVTTSNYANWVQEK 60
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Qy   61  PDHLFTGLIGGTSNRAPGVPVRFSGSSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFG 120
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Db   61  PDHLFTGLIGGTNRAPGVPARFSGSSLIGDKAALTITGAQTEDEATYFCALWYSNHWVFG 120

Qy  121  GGTKVTVL 128
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Db  121  GGTKLTVL 128
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RESULT 2
PCT-US95-15716-2
Sequence 2, Application PC/TUS951571G
; GENERAL INFORMATION:
; APPLICANT: Berdoz, Jose
; APPLICANT: Kraehenbuhl, Jean Pierre
; TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
; TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15716
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,548
; FILING DATE: 01-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06132/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-5070
; TELEX: 200154
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-15716-2

Query Match 89.4%; Score 597; DB 4; Length 128;
Best Local Similarity 90.6%; Pred. No. 4.4e-50;
Matches 116; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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Db    1  MAWISLILSLLALSSGAISQAVVTQESALTTSPGETVILTCRSSTGAVTTSNYANWVQEK 60

Qy   61  PDHLFTGLIGGTSNRAPGVPVRFSGSSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFG 120
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Db   61  PDHLFTGLIGGTNRAPGVPARFSGSSLIGDKAALTITGAQTEDEATYFCALWYSNHWVFG 120

Qy  121  GGTKVTVL 128
             |||||:|||
Db  121  GGTKLTVL 128
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RESULT 3
5215889-3
; Patent No. 5215889

; APPLICANT: SCHULTZ, PETER
; TITLE OF INVENTION: CATALYTIC AND REACTIVE POLYPEPTIDES
; TITLE OF INVENTION: AND METHODS FOR THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/404,920
; FILING DATE: 08-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 273,455
; FILING DATE: 18-NOV-1988
; SEQ ID NO:3:
; LENGTH: 115
5215889-3

Query Match 82.6%; Score 552; DB 6; Length 115;
Best Local Similarity 95.4%; Pred. No. 8.2e-46;
Matches 104; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db    2  AVVTQESALTTSPGTVILTCRSSTGAVTTSNYANWIQEKPDHLFTGLIGGTSNRAPGVP 61

Qy   81  VRFSGSSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFGGGGTKVTVLG 129
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Db   62  VRFSGSSLIGDKAALTITGAQTEDDAMYFCALWFRNHFVFGGGGTKVTVLG 110
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RESULT 4
US-08-428-257A-72
Sequence 72, Application US/08428257A
; Patent No. 5885808
; GENERAL INFORMATION:
; APPLICANT: Spooner, Robert A.
; APPLICANT: Epenetos, A.A.
; TITLE OF INVENTION: Compounds to target cells
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E. Goldberg
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,257A
; FILING DATE: 07/05/95
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-428-257A-72

Query Match 81.6%; Score 545; DB 1; Length 269;
Best Local Similarity 90.4%; Pred. No. 1.1e-44;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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Db  154  GGGSQAVVTQESALTTSPGETVILTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNR 213

Qy   76  APGVPVRFSGSSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFGGGGTKVTVLG 129
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Db  214  APGVPARFSGSSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGGTKLTVLG 267
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OM protein - protein search, using sw model

GenCore version 5.1.7
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Perfect score: 668
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Database :   Published Applications AA Main:*
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	668	100.0	129	4	US-10-768-193-8	Sequence 8, Appli
2	535	80.1	112	5	US-10-816-938-8	Sequence 8, Appli
3	531	79.5	110	5	US-10-816-938-21	Sequence 21, Appl
4	519	77.7	110	4	US-10-774-076-5	Sequence 5, Appl
5	513	76.8	110	4	US-10-350-555-1	Sequence 1, Appli
6	513	76.8	110	4	US-10-625-047-1	Sequence 1, Appli
7	513	76.8	110	4	US-10-631-258-1	Sequence 1, Appli
8	513	76.8	110	5	US-10-854-735-1	Sequence 1, Appli
9	513	76.8	110	5	US-10-835-533-1	Sequence 1, Appli
10	510	76.3	108	4	US-10-305-268-4	Sequence 4, Appli
11	510	76.3	391	4	US-10-328-190-14	Sequence 14, Appl
12	508	76.0	109	4	US-10-350-555-21	Sequence 21, Appl
13	508	76.0	109	4	US-10-350-555-29	Sequence 29, Appl
14	508	76.0	109	4	US-10-625-047-21	Sequence 21, Appl
15	508	76.0	109	4	US-10-625-047-29	Sequence 29, Appl
16	508	76.0	109	4	US-10-631-258-21	Sequence 21, Appl
17	508	76.0	109	5	US-10-854-735-21	Sequence 21, Appl
18	508	76.0	109	5	US-10-835-533-21	Sequence 21, Appl
19	508	76.0	109	5	US-10-631-258-29	Sequence 29, Appl
20	505	75.6	109	4	US-10-350-555-22	Sequence 22, Appl
21	505	75.6	109	4	US-10-625-047-22	Sequence 22, Appl
22	505	75.6	109	4	US-10-631-258-22	Sequence 22, Appl
23	505	75.6	109	5	US-10-854-735-22	Sequence 22, Appl
24	505	75.6	109	5	US-10-835-533-22	Sequence 22, Appl
25	505	75.6	109	4	US-10-350-555-27	Sequence 27, Appl
26	505	75.6	218	4	US-10-625-047-27	Sequence 27, Appl
27	505	75.6	218	5	US-10-631-258-27	Sequence 27, Appl
28	504	75.4	109	4	US-10-350-555-23	Sequence 23, Appl
29	504	75.4	109	4	US-10-625-047-23	Sequence 23, Appl
30	504	75.4	109	5	US-10-631-258-23	Sequence 23, Appl
31	504	75.4	109	5	US-10-854-735-23	Sequence 23, Appl
32	504	75.4	109	5	US-10-835-533-23	Sequence 23, Appl
33	504	75.4	218	4	US-10-350-555-28	Sequence 28, Appl
34	504	75.4	218	4	US-10-625-047-28	Sequence 28, Appl
35	495.5	75.4	218	4	US-10-631-258-28	Sequence 28, Appl
36	495.5	74.2	109	3	US-10-865-483-7	Sequence 7, Appli
37	495	74.1	218	5	US-10-726-555-7	Sequence 7, Appli
38	490	73.4	107	4	US-10-379-392-159	Sequence 159, App
39	490	72.8	109	3	US-10-940-727B-1	Sequence 1, Appli
40	486	72.8	109	4	US-10-328-190-10	Sequence 10, Appl
41	477	71.4	109	3	US-10-940-727B-2	Sequence 2, Appli
42	477	71.4	109	4	US-09-940-727B-3	Sequence 3, Appli
43	469	70.2	218	3	US-10-379-392-161	Sequence 161, App
44	460	68.9	218	4	US-10-379-392-164	Sequence 164, App
45	460	68.9	218	4	US-10-379-392-164	Sequence 164, App

ALIGNMENTS

RESULT 1
US-10-768-193-8
Sequence 8, Application US/10768193
; Publication No. US20040181042A1
; GENERAL INFORMATION:
; APPLICANT: MEDICAL & BIOLOGICAL LABORATORIES CO., LTD.
; APPLICANT: The director of Chubu National Hospital
; APPLICANT: YANAGISAWA, Katsuhiko
; APPLICANT: SHIBATA, Masao
; TITLE OF INVENTION: Antibody recognizing GM1 ganglioside-bound
;   amyloid b-protein and DNA encoding the antibody
; FILE REFERENCE: P0102402
; CURRENT APPLICATION NUMBER: US/10/768,193
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: JP P2001-235700
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: PCT/JP02/07874
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 8
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-768-193-8

Query Match   100.0%; Score 668; DB 4; Length 129;
Best Local Similarity   100.0%; Pred. No. 2.8e-55;
Matches 129; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MAWTSLILSLLALCSGASSQAVVTQESALTTSPGGTVILTCRSSTGAVTTSNYANWVQEK 60
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Db   1 MAWTSLILSLLALCSGASSQAVVTQESALTTSPGGTVILTCRSSTGAVTTSNYANWVQEK 60

Qy   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFG 120
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Db   61 PDHLFTGLIGGTSNRAPGVPVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFG 120

Qy   121 GGTKVTVLG 129
              |||||||||
Db   121 GGTKVTVLG 129

RESULT 2
US-10-816-938-8
Sequence 8, Application US/10816938
; Publication No. US20040229301A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Baiyang
; TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof

; FILE REFERENCE: 1861.1670002
; CURRENT APPLICATION NUMBER: US/10/816,938
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.2
US-10-816-938-8
; SEQ ID NO 8
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.

Query Match   80.1%; Score 535; DB 5; Length 112;
Best Local Similarity 91.8%; Pred. No. 8.7e-43;
Matches 101; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 60

Qy  80 PVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFGGGTKVTVLG 129
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Db  61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHVFGGGTKLTVLG 110
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RESULT 3
US-10-816-938-21
; Sequence 21, Application US/10816938
; Publication No. US20040229301A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Baiyang
; TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof
; FILE REFERENCE: 1861.1670002
; CURRENT APPLICATION NUMBER: US/10/816,938
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 21
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-816-938-21

Query Match   79.5%; Score 531; DB 5; Length 110;
Best Local Similarity 90.9%; Pred. No. 2e-42;
Matches 100; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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Qy  80 PVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFGGGTKVTVLG 129
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Db  61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHVFGGGTKLTVLG 110
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RESULT 4
US-10-774-076-5
; Sequence 5, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 110
; TYPE: PRT
; ORGANISM: mus sp.

US-10-774-076-5

Query Match   79.5%; Score 531; DB 5; Length 110;
Best Local Similarity 90.9%; Pred. No. 2e-42;
Matches 100; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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Qy  20 QAVVTQESALTTSPGGTVILTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTSNRAPGV 79
          ||||||||||||||| || |||||||||||||||||||||||||||||||||| || |||
Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRPGV 60

Qy  80 PVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFGGGTKVTVLG 129
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Db  61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHVFGGGTKLTVLG 110
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RESULT 5
US-10-350-555-1
; Sequence 1, Application US/10350555
; Publication No. US20040146934A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Corneillie, Todd
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 023070-13090US
; CURRENT APPLICATION NUMBER: US/10/350,555
; CURRENT FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: murine monoclonal antibody 2D12.5 light chain
; OTHER INFORMATION: variable domain (VL)
US-10-350-555-1

Query Match   77.7%; Score 519; DB 4; Length 110;
Best Local Similarity 90.0%; Pred. No. 2.8e-41;
Matches 99; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINNRVPGV 60

Qy  80 PVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFGGGTKVTVLG 129
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Db  61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHVFGGGTKLTVLG 110
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RESULT 6
US-10-625-047-1
; Sequence 1, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Corneillie, Todd
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 023070-13091US
; CURRENT APPLICATION NUMBER: US/10/625,047
; PRIOR APPLICATION NUMBER: US 10/350,555
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: murine monoclonal antibody 2D12.5 light chain

Query Match   76.8%; Score 513; DB 4; Length 110;
Best Local Similarity 87.3%; Pred. No. 1e-40;
Matches 96; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

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Qy  20 QAVVTQESALTTSPGGTVILTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTSNRAPGV 79
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Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRPGV 60

Qy  80 PVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFGGGTKVTVLG 129
          | ||||||||||||||: | :|||||||:||:|||||||:|||||||:|||
Db  61 PARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHVFGGGTRLTVLG 110
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OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: March 21, 2006, 18:07:45 ; Search time 14.117 Seconds
                                                  (without alignments)
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Title:
Perfect score: 668
Sequence: 1 MAWTSLILSLLALCSGASSQ............ALWYSTHYVFGGGTKVTVLG 129

Scoring table: BLOSUM62
                       Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   Published Applications AA_New:*
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                  4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                  5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*-
                  6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                  7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                  8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB ID	Description
1	495.5	74.2	109	6	US-10-726-554-7	Sequence 7, Appli
2	444.5	66.5	109	7	US-11-100-553B-37	Sequence 37, Appl
3	437.5	65.5	109	7	US-11-100-553B-36	Sequence 36, Appl
4	350	52.4	245	7	US-11-054-515-1523	Sequence 1523, Ap
5	329.5	49.3	240	7	US-11-000-463-248	Sequence 248, App
6	327.5	49.0	249	7	US-11-054-515-1838	Sequence 1838, Ap
7	323	48.4	108	7	US-11-064-174-51	Sequence 51, Appl
8	323	48.4	108	7	US-11-064-174-52	Sequence 52, Appl
9	321	48.1	108	7	US-11-064-174-166	Sequence 166, Appl
10	315.5	47.2	111	7	US-11-155-775-36	Sequence 36, Appl
11	312.5	46.8	251	7	US-11-054-515-890	Sequence 890, App
12	312.5	46.8	251	7	US-11-054-515-891	Sequence 891, App
13	312.5	46.8	251	7	US-11-054-515-894	Sequence 894, App
14	312.5	46.8	251	7	US-11-054-515-903	Sequence 903, App
15	312.5	46.8	251	7	US-11-054-515-910	Sequence 910, App
16	312.5	46.8	251	7	US-11-054-515-1121	Sequence 1121, Ap
17	312.5	46.8	251	7	US-11-054-515-1126	Sequence 1126, Ap
18	312.5	46.8	251	7	US-11-054-515-1140	Sequence 1140, Ap
19	312.5	46.8	251	7	US-11-054-515-1141	Sequence 1141, Ap
20	312.5	46.8	251	7	US-11-054-515-1147	Sequence 1147, Ap
21	312.5	46.8	251	7	US-11-054-515-1148	Sequence 1148, Ap
22	312.5	46.8	251	7	US-11-054-515-1157	Sequence 1157, Ap
23	312.5	46.8	251	7	US-11-054-515-1162	Sequence 1162, Ap
24	312.5	46.8	251	7	US-11-054-515-1373	Sequence 1373, Ap
25	311	46.6	119	7	US-11-000-463-720	Sequence 720, App
26	309.5	46.3	251	7	US-11-054-515-1127	Sequence 1127, Ap
27	307	46.0	108	7	US-11-064-174-53	Sequence 53, Appl
28	305.5	45.7	251	7	US-11-054-515-1151	Sequence 1151, Ap
29	301.5	45.1	251	7	US-11-054-515-1166	Sequence 1166, Ap
30	296.5	44.4	251	7	US-11-054-515-1152	Sequence 1152, Ap
31	291	43.6	98	7	US-11-084-554-219	Sequence 219, App
32	291	.98	98	7	US-11-136-250-219	Sequence 219, App
33	287	43.0	98	7	US-11-084-554-220	Sequence 220, App
34	287	43.0	98	7	US-11-136-250-220	Sequence 220, App
35	281.5	42.1	98	7	US-11-084-554-221	Sequence 221, App
36	275.5	41.2	253	7	US-11-054-515-1149	Sequence 1149, Ap
37	270	40.4	232	7	US-11-136-250-221	Sequence 221, App
38	267.5	40.0	231	7	US-11-000-463-283	Sequence 283, App
39	265.5	39.7	249	7	US-11-054-515-1312	Sequence 1312, Ap
40	264.5	39.6	244	7	US-11-054-515-1842	Sequence 1842, Ap
41	264	39.5	99	7	US-11-084-554-221	Sequence 221, App
42	264	39.5	99	7	US-11-136-250-221	Sequence 221, App
43	261	39.1	253	7	US-11-054-515-1364	Sequence 1364, App
44	259	38.8	236	7	US-11-000-463-815	Sequence 815, App
45	255	38.2	245	7	US-11-054-515-1864	Sequence 1864, Ap

ALIGNMENTS

RESULT 1
US-10-726-554-7
; Sequence 7, Application US/10726554
; Publication No. US2005024973A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong Wook et al.
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST
; TITLE OF INVENTION: THE HBV S-SURFACE
; TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
; FILE REFERENCE: 1599-0197P
; CURRENT APPLICATION NUMBER: US/10/726,554·
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US/09/865,483
; PRIOR FILING DATE: 2001-03-29

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-726-554-7

  Query Match   74.2%; Score 495.5; DB 6; Length 109;
  Best Local Similarity   85.5%; Pred. No. 1.5e-35;
  Matches   94; Conservative   10; Mismatches   5; Indels   1; Gaps   1;

Qy   20 QAVVTQESALTTSPGGTVILTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTSNRAPGV 79
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Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAITTNNFANWVQEKPDHLFTGLIGDTNNRVPGV 60

Qy   80 PVRFSGSLLGDKAALTITGAQTEDDAMYFCALWYSTHYVFGGGTKVTVLG 129
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Db   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWIN-NWFGGGTKLITVLG 109

RESULT 2
US-11-100-553B-37
; Sequence 37, Application US/11100553B
; Publication No. US2006001493A1
; GENERAL INFORMATION:
; APPLICANT: Heui Il, KANG, et al.
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST S-SURFACE ANTIGEN OF HEPATITIS B VIRUS
; FILE REFERENCE: Q87350
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST S-SURFACE ANTIGEN OF HEPATITIS B VIRUS
; CURRENT APPLICATION NUMBER: US/11/100,553B
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: KR10-2004-25573
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 43

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; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 37
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variable region of humanized light chain LFW22-312
US-11-100-553B-37

Query Match     66.5%;  Score 444.5;  DB 7;  Length 109;
Best Local Similarity   76.4%;  Pred. No. 3e-31;
Matches   84;  Conservative   12;  Mismatches   13;  Indels   1;  Gaps   1;

Qy   20  QAVVTQESALTTSPGGTVILTCRSSTGAVTTSNYANWVQEKPDHLFTGLLIGGTSNRAPGV  79
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Db    1  QAAVTQEPSLTVSPGGTVTLTCRSSTGAITTNNFANWFQQKPGQAFRGLIGDTNNRVPGV   60

Qy   80  PVRFSGSLLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFGGGTKVTVLG  129
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Db   61  PARFSGSSLIGDKAALITTGAQPEDEAEYCALWYN-NWVFGGGTKLTVLG  109
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RESULT 3
US-11-100-553B-36
; Sequence 36, Application US/11100553B
; Publication No. US20060014937A1
; GENERAL INFORMATION:
; APPLICANT: Heui Il, KANG, et al.
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST S-SURFACE ANTIGEN OF HEPATITIS B VIRUS
; FILE REFERENCE: Q87350
; CURRENT APPLICATION NUMBER: US/11/100,553B
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: KR10-2004-25573
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 36
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variable region of humanized light chain LFW22-31
US-11-100-553B-36

Query Match     65.5%;  Score 437.5;  DB 7;  Length 109;
Best Local Similarity   74.5%;  Pred. No. 1.2e-30;
Matches   82;  Conservative   14;  Mismatches   13;  Indels   1;  Gaps   1;

Qy   20  QAVVTQESALTTSPGGTVILTCRSSTGAVTTSNYANWVQEKPDHLFTGLLIGGTSNRAPGV  79
             |||||||||||:|||||||||||||||||:||:|||:||:||||| :||||||||
Db    1  QAAVTQEPSLTVSPGGTVTLTCRSSTGAITTNNFANWFQQKPGQAFRGLIGDTNNRVPGV   60

Qy   80  PVRFSGSLLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFGGGTKVTVLG  129
             :|||||||:||||| |:||||:|||:||||||||: |||||||||| ||||
Db   61  PARFSGSSLIGNKAALITTGAQPEDEAEYCALWYN-NWVFGGGTKLTVLG  109
```

```
RESULT 4
US-11-054-515-1523
; Sequence 1523, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296.
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1523
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1523

Query Match     52.4%;  Score 350;  DB 7;  Length 245;
Best Local Similarity   60.3%;  Pred. No. 6.5e-23;
Matches   70;  Conservative   13;  Mismatches   31;  Indels   2;  Gaps   1;

Qy   16  GASSQAVVTQESALTTSPGGTVILTCRSSTGAVTTSNYANWVQEKPDHLFTGLLIGGTSNR   75
             |:| |||:|||||||||||||:||:|| :||:|||:| :||:|||| :|| |:
Db  130  GGSAQVVIQEPSLTVSPGGTVTLTCASITGAVTSGNYPNWFQQKPGQAFRALIYSTDNK   189

Qy   76  APGVPVRFSGSLLIGDKAALTITGAQTEDDAMYFCALWY--STHYVFGGGTKVTVLG  129
             ||:|:|||||| :|||||||| |::|||||:||| |   |||||||||||||| ||
Db  190  HSWTPARFSGSSLIGDKAALTLSGVQPEDEAEYCLLYYGGAQPWVRGGGTKVTVLG  245
```

```
RESULT 5
US-11-000-463-248
; Sequence 248, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; CURRENT APPLICATION NUMBER: US/11/000,463
; FILE REFERENCE: 785CIP4CN
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 248
; LENGTH: 240
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